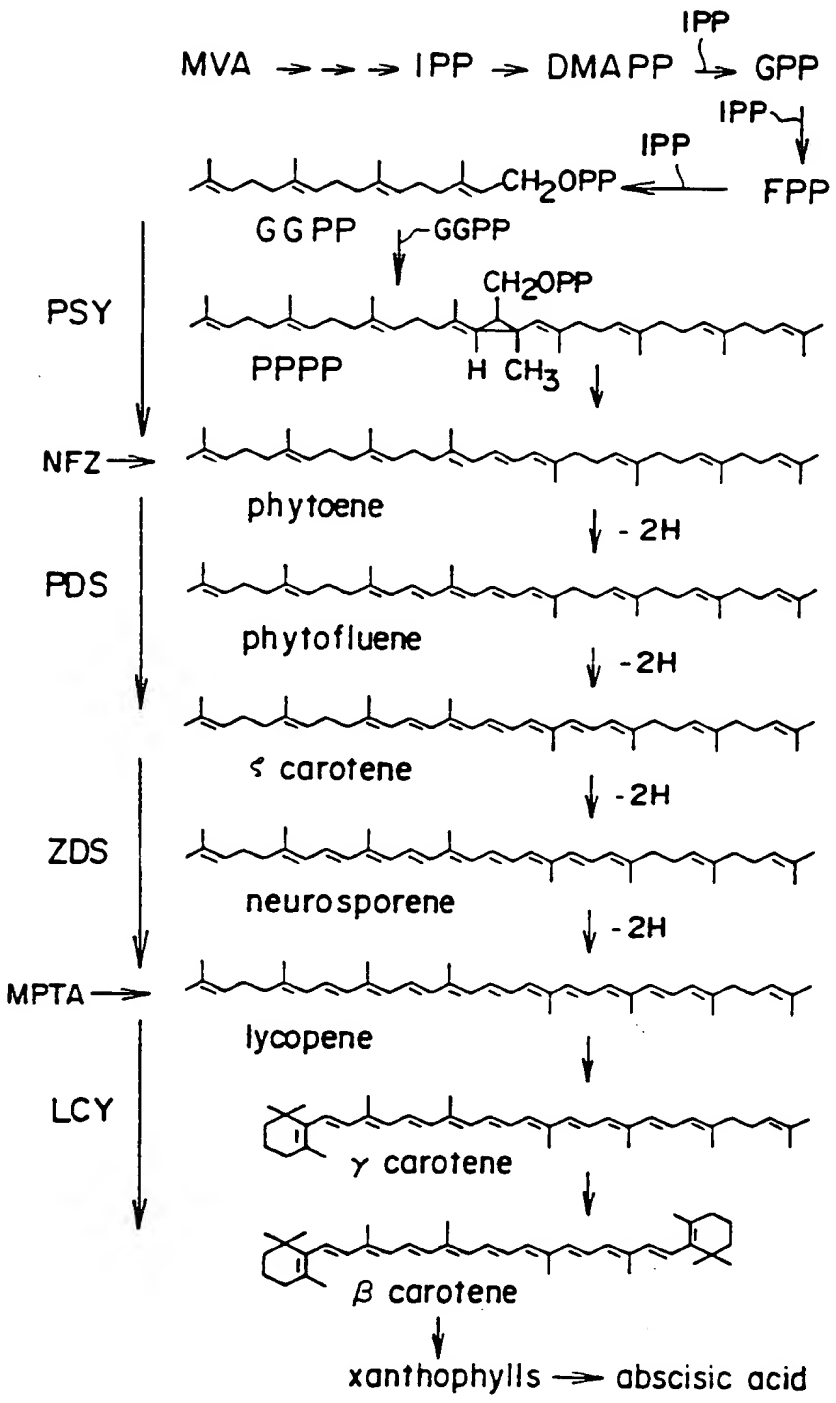

FIG. 1

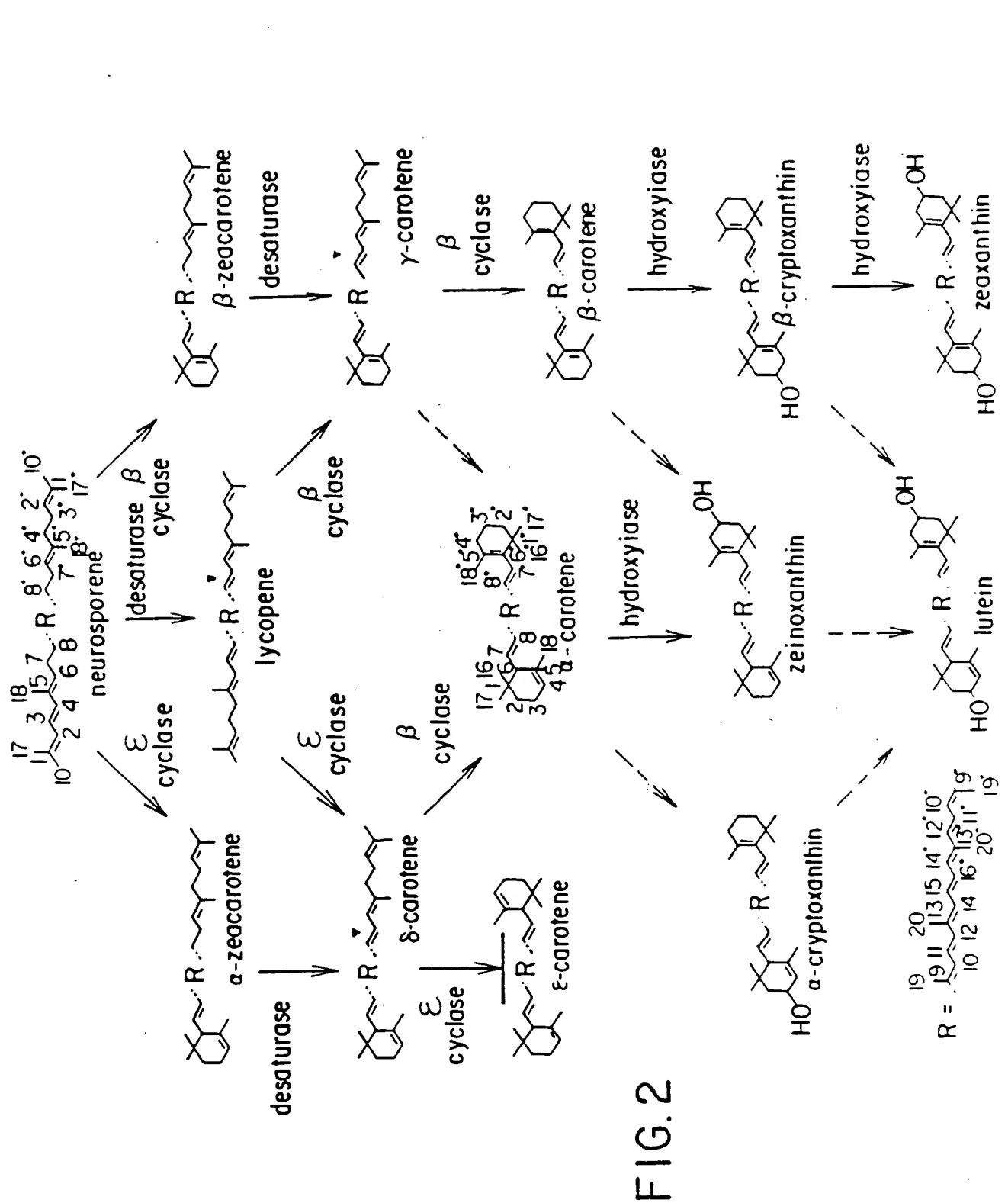

FIG. 2

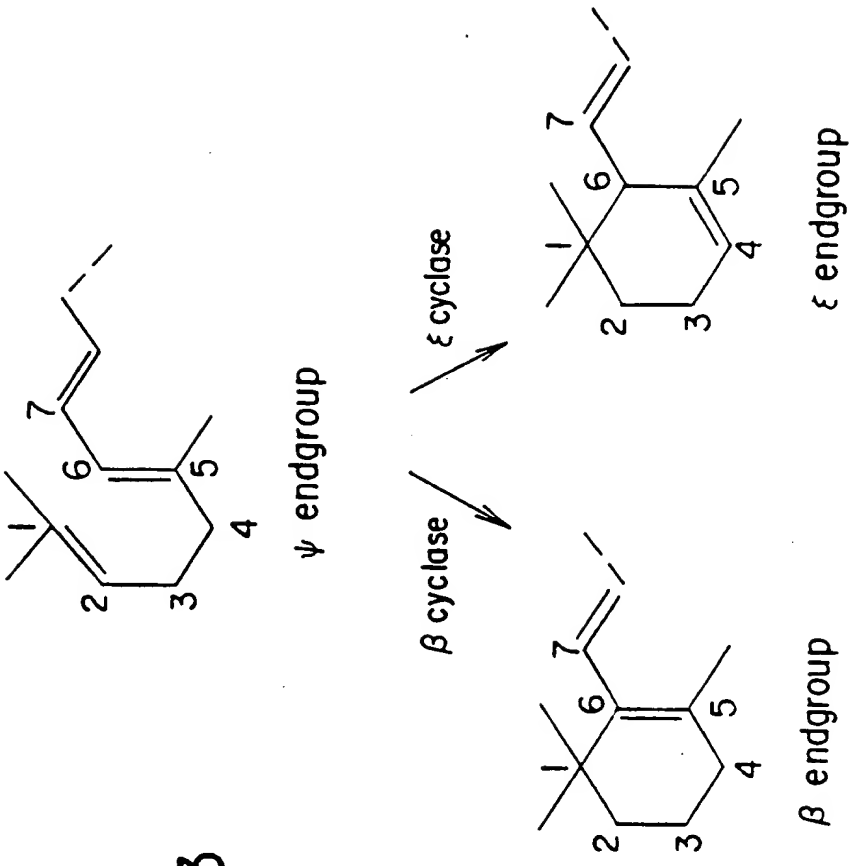

FIG. 3

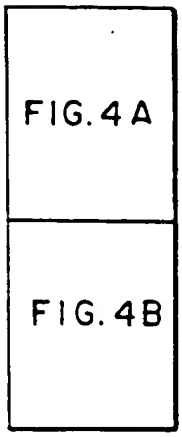

FIG. 4

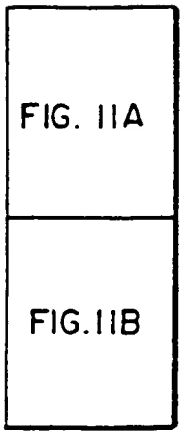

FIG. 11

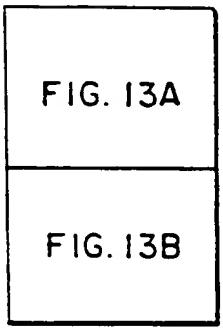

FIG. 13

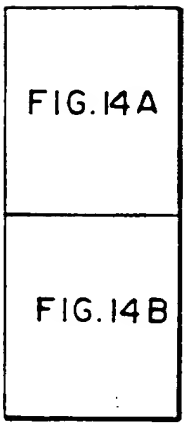

FIG. 14

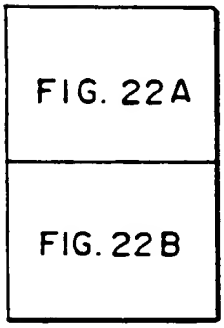

FIG. 22

FIG. 4A

Arabidopsis thaliana epsilon cyclase:

```
                                acaaaaggaaataattag attcctctttctgcttgctataccttgaca  48
      gaacaacataacaatggtgtaagtcttctc gctgtattcgaaattatttggaggaggaac 108
      atggagtgtgttggggctaggaatttcgca gcaatggcggtttcaacatttccgtcatgg 168
    1 M  E  C  V  G  A  R  N  F  A  A  M  A  V  S  T  F  P  S  W
      agttgtcgaaggaaatttccagtggctaag agatacagctataggaatattcgcttcggt 228
   21 S  C  R  R  K  F  P  V  V  K  R  Y  S  Y  R  N  I  R  F  G
      ttgtgtagtgtcagagctagcggcggcgga agttccggtagtgagagttgtgtagcggtg 288
   41 L  C  S  V  R  A  S  G  G  G  S  S  G  S  K  S  C  V  A  V
      agagaagatttcgctgacgaagaagatttt gcgaaagctggcggttctgagattctattt 348
   61 R  S  D  F  A  D  E  E  D  F  V  E  A  G  G  S  R  I  L  F
      gttcaaatgcagcagaacaaagatatggat gaacagtctaagcttgttgataagttgcct 408
   81 V  Q  M  Q  Q  M  K  D  M  D  S  Q  S  K  L  V  D  K  L  P
      cctatatcaactggtgatggtgctttggat catgtggttactggctgtggtcctgctggt 468
  101 P  I  S  I  G  D  G  A  L  D  K  V  V  I  G  C  G  P  A  G
      ttagccttggctgcagaatcagctaagctt ggattaaaagttggactcattggtccagat 528
  121 L  A  L  A  A  K  S  A  K  L  G  L  K  V  G  L  I  G  P  D
      cttccttttactaacaattacggtgtttgg gaagatgaattcaatgatcttgggctgcaa 588
  141 L  P  F  T  M  M  Y  G  V  M  K  D  K  F  N  D  L  G  L  G
      aaatgtattgagcatgtttggagagagact attgcgcacctggatgatgacaagcctatt 648
  161 K  C  I  K  K  V  W  R  S  T  I  V  Y  L  D  D  D  K  P  I
      accattggccgtgcttatggaagagttagt cgacgtttgctccatgaggagcttttgagg 708
  181 T  I  G  R  A  Y  G  R  V  S  R  R  L  L  X  E  E  L  L  R
      aggtgtgtcgagtcaggtgtctcgtacctt agctcgaaagttgacagcataacagaagct 768
  201 R  C  V  K  S  G  V  S  Y  L  S  S  K  V  D  S  I  T  E  A
      tgtgatggccttagacttgttgcttgtgac gacaataacgtcattccctgcaggcttgcc 828
  221 S  D  G  L  X  L  V  A  C  D  D  M  M  V  I  P  C  X  L  A
      actgttgcttctggagcagcttcgggaaag ctcttgcaatacgaagttggtggacctaga 888
  241 T  V  A  S  G  A  A  S  G  K  L  L  Q  Y  X  V  G  G  P  R
      gtctgtgcgcaaactgcatacggcgtggag gttgaggcggaaaatagtccatatgatcca 948
```

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O.G. FIG. | CLASS | SUBCLASS
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FIG. 4B

261 V C V Q T A Y G V X V X V X N S P Y D P

gatcaaatggttttcatggattacagagat tatactaacgagaaagttcggagcttagaa 1008
281 D Q M V P M D Y R D Y T M X X V R S L X

gctgagtatccaacgtttctgtacgccatg cctatgacaaagtcaagactcttcttcgag 1068
301 A K Y P T F L Y A M P M T K S R L F F K

gagacatgtttggcctcaaaagatgtcatg ccctttgatttgctaaaaacgaagctcatg 1128
321 K T C L A S K D V M P F D L L K T K L M

ttaagattagacacactcggaattcgaatt ctaaagacttacgaagaggagtggtcctat 1188
341 I P V G G S L P N T X Q K N L A F G A A

atcccagttggtggttccttgccaaacacc gaacaaaagaatctcgcctttggtgctgcc 1248
361 I P V G G S L P M T X Q K N L A F G A A

gctagcatggtacatcccgcaacaggctat tcagttgtgagatctttgtctgaagctcca 1308
381 A S M V M P A T G Y S V V R S L S X A P

aaacatgcatcagtcatcgcagagatacta agagaagagactaccaaacagattaacagt 1368
401 K Y A S V I A K I L R E E T T K Q I N S

aatatttcaagacaagcttaggatacttta tggccaccagaaaggaaaagacagagagca 1428
421 M I S R Q A W D T L W P P E R X R Q R A

ttctttctctttggtcttgcactcagagtt caattcgataccgaaggcattagaagcttc 1488
441 F F L F G L A L I V Q F D T X G I R S F

ttccgtactttcttccgccttccaaaatgg atgtggcaagggtttctaggatcaacatta 1548
461 F R T P F R L P K W M W Q G F L G S T L

acatcaggagatctcgttctctttgcttta tacatgttcgtcatttcaccaaacaatttg 1608
481 T S G D L V L F A L Y M P V I S P M M L

agaaaaggtctcattaatcatctcatctct gatccaaccggagcaaccatgataaaaacc 1668
501 R K G L I N W L I S D P T G A T M I K T

tatctcaaagtatgatttacttaccaactc ttaggtttgtgtatatatatgccgatttat 1728

521 Y L K V

ctgaataatcgatcaaagaatggtatgtgg gttactaggaagttggaaacaaacacgtat 1788

agaatctaaggagtgatcgaaatggagacg gaaacgaaaagaaaaaaatcagtctttgtt 1848

ccgtggctagtg 1868

FIG. 5

```
   1  gctctttctc ctcctcctct accgatttcc gactccgcct cccgaaatcc
  51  ttatccggat tctctccgtc tcttcgattt aaacgctttt ctgtctgtta
 101  cgtcgtcgaa gaacggagac agaattctcc gattgagaac gatgagagac
 151  cggagagcac gagctccaca aacgctatag acgctgagta tctggcgttg
 201  cgtttggcgg agaaattgga gaggaagaaa tcggagaggt ccacttatct
 251  aatcgctgct atgttgtcga gctttggtat cacttctatg gctgttatgg
 301  ctgtttacta cagattctct tggcaaatgg agggaggtga gatctcaatg
 351  ttggaaatgt ttggtacatt tgctctctct gttggtgctg ctgttggtat
 401  ggaattctgg gcaagatggg ctcatagagc tctgtggcac gcttctctat
 451  ggaatatgca tgagtcacat cacaaaccaa gagaaggacc gtttgagcta
 501  aacgatgttt ttgctatagt gaacgctggt ccagcgattg gtctcctctc
 551  ttatggattc ttcaataaag gactcgttcc tggtctctgc tttggcgccg
 601  ggttaggcat aacggtgttt ggaatcgcct acatgtttgt ccacgatggt
 651  ctcgtgcaca agcgtttccc tgtaggtccc atcgccgacg tcccttacct
 701  ccgaaaggtc gccgccgctc accagctaca tcacacagac aagttcaatg
 751  gtgtaccata tggactgttt cttggaccca aggaattgga agaagttgga
 801  ggaaatgaag agttagataa ggagattagt cggagaatca aatcatacaa
 851  aaaggcctcg ggctccgggt cgagttcgag ttcttgactt taaacaagtt
 901  ttaaatccca aattcttttt ttgtcttctg tcattatgat catcttaaga
 951  cggtct
```

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FIG. 6

```
                                                                                                        64
A.thal.                SFSS SSTDFRLRLP KSLSGFSPSL RFKRFSVCYV VEERRQNSPI ENDERPESTS STNAIDAEYL

                                                                                                       144
A.thal.    ALRLAEKLER KKSERSTYLI AAMLSSFGIT SMAVMAVYYR FSWQMEGGEI SMLEMFGTFA LSVGAAVGME FWARWAHRAL
Alical.    .......... .......... .......... .......... .......... .....MTQFL IVVATVLVME LTAYSVHRWI
A.aurant.  .......... .......... .......... .......... .......... .....MTNFL IVVATVLVME LTAYSVHRWI
E.herb.    .......... .......... .......... .......... .......... ....ML.NSL IVILSVIAME GIAAFTHRYI
E.ured.    .......... .......... .......... .......... .......... ..MLWIWNAL IVIVTVIGME VIAALAHKYI
Consensus  ---------- ---------- ---------- ---------- ---------- --------f- --v-----ME --A---Hr--

                      Predicted TM helix                      Predicted TM helix

                                                                                                       224
A.thal.    WHASL.WNMH ESHHKPREGP FELNDVFAIV NAGPAIGLLS YGFFNKGLVP GLCFGAGLGI TVFGIAYMFV HDGLVHKRFP
Alical.    MHGPLGWGWH KSHHEEHDHA LEKNDLYGVV FAVLATILFT VGAYWWPVLW WI....ALGM TVYGLIYFIL HDGLVHQRWP
A.aurant.  MHGPLGWGWH KSHHEEHDHA LEKNDLYGLV FAVIATVLFT VGWIWAPVLW WI....ALGM TVYGLIYFVL HDGLVHQRWP
E.herb.    MHG.WGWRWH ESHHTPRKGV FKLNDLFAVV FAGVAIALIA VGTAGVWPLQ WI....GCGM TVYGLLYFLV HDGLVHQRWP
E.ured.    MHG.WGWGWH LSHHEPRKGA FEVNDLYAVV FAALSILLIY LGSTGMWPLQ WI....GAGM TAYGLLYFMV HDGLVHQRWP
Consensus  -H--l-W--H -SHH-pr-g- fE-ND--a-V -A--ai-L-- -G-------- ------glG- Tv-G--Y--v HDGLVH-R-P

                              Predicted TM helix          Predicted TM helix

                                                                                                 301
A.thal.    VGPIADVPYL RKVAAAHQLH HT..DKFNGV PYGLFLGPKE LEEVGGNEEL DKEISRRIKS YKKASGSGSS SSS*...
Alical.    FRYIPRRGYF RRLYQAHRLH HAVEGRDHCV SFGFIYAPP. VDKLKQDLKR SGVLRPQDER PS*....... .......
A.aurant.  FRYIPRKGYA RRLYQAHRLH HAVEGRDHCV SFGFIYAPP. VDKLKQDLKM SGVLRAEAQE RT*....... .......
E.herb.    FHWIPRRGYL KRLYVAHRLH HAVRGREGCV SFGFIYARK. PADLQAILRE RHGRPPKRDA AKDRPDAASP SSSSPE*
E.ured.    FRYIPRKGYL KRLYMAHRMH HAVRGKEGCV SFGFLYAPP. LSKLQATLRE RHG..ARAGA ARDAQGGEDE PASGK*.
Consensus  ---I----Yl r----AH-lH H--------V --G----p-- ---------- ---------- ---------- --s----
```

FIG. 7

```
   1  ccacgggtcc gcctcccccgt ttttttccga tccgatctcc ggtgccgagg
  51  actcagctgt ttgttcgcgc tttctcagcc gtcaccatga ccgattctaa
 101  cgatgctgga atggatgctg ttcagagacg actcatgttt gaagacgaat
 151  gcattctcgt tgatgaaaat aatcgtgtgg tgggacatga cactaagtat
 201  aactgtcatc tgatggaaaa gattgaagct gagaatttac ttcacagagc
 251  tttcagtgtg tttttattca actccaagta tgagttgctt ctccagcaac
 301  ggtcaaaaac aaaggttact ttcccacttg tgtggacaaa cacttgttgc
 351  agccatcctc tttaccgtga atccgagctt attgaagaga atgtgcttgg
 401  tgtaagaaat gccgcacaaa ggaagctttt cgatgagctc ggtattgtag
 451  cagaagatgt accagtcgat gagttcactc ccttgggacg catgctttac
 501  aaggcacctt ctgatgggaa atggggagag cacgaagttg actatcttact
 551  cttcatcgtg cgggatgtga agcttcaacc aaacccagat gaagtggctg
 601  agatcaagta cgtgagcagg gaagagctta aggagctggt gaagaaagca
 651  gatgctggcg atgaagctgt gaaactatct ccatggttca gattggtggt
 701  ggataatttc ttgatgaagt ggtgggatca tgttgagaaa ggaactatca
 751  ctgaagctgc agacatgaaa accattcaca agctctgaac tttccataag
 801  ttttggatct tccccttccc ataataaaat taagagatga gacttttatt
 851  gattacagac aaaactggca acaaaatcta ttcctaggat ttttttttgc
 901  tttttattta cttttgattc atcttctagtt tagttttcat cttaaaaaaa
 951  aaaa
```

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FIG. 8

```
  1 caccaatgtc tgtttcttct ttatttaatc tcccattgat tcgcctcaga
 51 tctctcgctc tttcgtcttc tttttcttct ttccGATTTG CCCATCGTCC
101 TCTGTCATCG ATTTCACCGA GAAAGTTACC GAATTTTCGT GCTTTCTCTG
151 GTACCGCTAT GACAGATACT AAAGATGCTG GTATGGATGC TGTTCAGAGA
201 CGTCTCATGT TTGAGGATGA ATGCATTCTT GTTGATGAAA CTGATCGTGT
251 TGTGGGGCAT GTCAGCAAGT ATAATTGTCA TCTGATGGAA AATATTGAAG
301 CCAAGAATTT GCTGCACAGG GCTTTTAGTG TATTTTTATT CAACTCGAAG
351 TATGAGTTGC TTCTCCAGCA AAGGTCAAAC ACAAAGGTTA CGTTCCCTCT
401 AGTGTGGACT AACACTTGTT GCAGCCATCC TCTTTACCGT GAATCAGAGC
451 TTATCCAGGA CAATGCACTA GGTGTGAGGA ATGCTGCACA AAGAAAGCTT
501 CTCGATGAGC TTGGTATTGT AGCTGAAGAT GTACCAGTCG ATGAGTTCAC
551 TCCCTTGGGA CGTATGCTGT ACAAGGCTCC TTCTGATGGC AAATGGGGAG
601 AGCATGAACT TGATTACTTG CTCTTCATCG TGCGAGACGT GAAGGTTCAA
651 CCAAACCCAG ATGAAGTAGC TGAGATCAAG TATGTGAGCC GGGAAGAGCT
701 GAAGGAGCTG GTGAAGAAAG CAGATGCAGG TGAGGAAGGT TTGAAACTGT
751 CACCATGGTT CAGATTGGTG GTGGACAATT TCTTGATGAA GTGGTGGGAT
801 CATGTTGAGA AAGGAACTTT GGTTGAAGCT ATAGACATGA AAACCATCCA
851 CAAACTCTGA ACATCTTTTT TTAAAGTTTT TAAATCAATC AACTTTCTCT
901 TCATCATTTT TATCTTTTCG ATGATAATAA TTTGGGATAT GTGAGACACT
951 TACAAAACTT CCAAGCACCT CAGGCAATAA TAAAGTTTGC GGCCGC
```

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FIG. 9

1 CTCGGTAGCT GGCCACAATC GCTATTTGGA ACCTGGCCCG GCGGCAGTCC

51 GATGCCGCGA TGCTTCGTTC GTTGCTCAGA GGCCTCACGC ATATCCCCCG

101 CGTGAACTCC GCCCAGCAGC CCAGCTGTGC ACACGCGCGA CTCCAGTTTA

151 AGCTCAGGAG CATGCAGATG ACGCTCATGC AGCCCAGCAT CTCAGCCAAT

201 CTGTCGCGCG CCGAGGACCG CACAGACCAC ATGAGGGGTG CAAGCACCTG

251 GGCAGGCGGG CAGTCGCAGG ATGAGCTGAT GCTGAAGGAC GAGTGCATCT

301 TGGTGGATGT TGAGGACAAC ATCACAGGCC ATGCCAGCAA GCTGGAGTGT

351 CACAAGTTCC TACCACATCA GCCTGCAGGC CTGCTGCACC GGGCCTTCTC

401 TGTGTTCCTG TTTGACGATC AGGGGCGACT GCTGCTGCAA CAGCGTGCAC

451 GCTCAAAAAT CACCTTCCCA AGTGTGTGGA CGAACACCTG CTGCAGCCAC

501 CCTTTACATG GGCAGACCCC AGATGAGGTG GACCAACTAA GCCAGGTGGC

551 CGACGGAACA GTACCTGGCG CAAAGGCTGC TGCCATCCGC AAGTTGGAGC

601 ACGAGCTGGG GATACCAGCG CACCAGCTGC CGGCAAGCGC GTTTCGCTTC

651 CTCACGCGTT TGCACTACTG TGCCGCGGAC GTGCAGCCAG CTGCGACACA

701 ATCAGCGCTC TGGGGCGAGC ACGAAATGGA CTACATCTTG TTCATCCGGG

751 CCAACGTCAC CTTGGCGCCC AACCCTGACG AGGTGGACGA AGTCAGGTAC

801 GTGACGCAAG AGGAGCTGCG GCAGATGATG CAGCCGGACA ACGGGCTGCA

851 ATGGTCGCCG TGGTTTCGCA TCATCGCCGC GCGCTTCCTT GAGCGTTGGT

901 GGGCTGACCT GGACGCGGCC CTAAACACTG ACAAACACGA GGATTGGGGA

951 ACGGTGCATC ACATCAACGA AGCGTGAAAG CAGAAGCTGC AGGATGTGAA

1001 GACACGTCAT GGGGTGGAAT TGCGTACTTG GCAGCTTCGT ATCTCCTTTT

1051 TCTGAGACTG AACCTGCAGT CAGGTCCCAC AAGGTCAGGT AAAATGGCTC

1101 GATAAAATGT ACCGTCACTT TTTGTCGCGT ATACTGAACT CCAAGAGGTC

1151 AAAAAAAAAA AAAAA

FIG. 10


```
   1  CTCGGTAGCT GGCCACAATC GCTATTTGGA ACCTGGCCCG GCGGCAGTCC
  51  GATGCCGCGA TGCTTCGTTC GTTGCTCAGA GGCCTCACGC ATATCCCGCG
 101  CGTGAACTCC GCCCAGCAGC CCAGCTGTGC ACACGCGCGA CTCCAGTTTA
 151  AGCTCAGGAG CATGCAGCTG CTTTCCGAGG ACCGCACAGA CCACATGAGG
 201  GGTGCAAGCA CCTGGGCAGG CGGGCAGTCG CAGGATGAGC TGATGCTGAA
 251  GGACGAGTGC ATCTTGGTAG ATGTTGAGGA CAACATCACA GGCCATGCCA
 301  GCAAGCTGGA GTGTCACAAG TTCCTACCAC ATCAGCCTGC AGGCCTGCTG
 351  CACCGGGCCT TCTCTGTGTT CCTGTTTGAC GATCAGGGGC GACTGCTGCT
 401  GCAACAGCGT GCACGCTCAA AAATCACCTT CCCAAGTGTG TGGACGAACA
 451  CCTGCTGCAG CCACCCTTTA CATGGGCAGA CCCCAGATGA GGTGGACCAA
 501  CTAAGCCAGG TGGCCGACGG AACAGTACCT GGCGCAAAGG CTGCTGCCAT
 551  CCGCAAGTTG GAGCACGAGC TGGGGATACC AGCGCACCAG CTGCCGGCAA
 601  GCGCGTTTCG CTTCCTCACG CGTTTGCACT ACTGTGCCGC GGACGTGCAG
 651  CCAGCTGCGA CACAATCAGC GCTCTGGGGC GAGCACGAAA TGGACTACAT
 701  CTTGTTCATC CGGGCCAACG TCACCTTGGC GCCCAACCCT GACGAGGTGG
 751  ACGAAGTCAG GTACGTGACG CAAGAGGAGC TGCGGCAGAT GATGCAGCCG
 801  GACAACGGGC TTCAATGGTC GCCGTGGTTT CGCATCATCG CCGCGCGCTT
 851  CCTTGAGCGT TGGTGGGCTG ACCTGGACGC GGCCCTAAAC ACTGACAAAC
 901  ACGAGGATTG GGGAACGGTG CATCACATCA ACGAAGCGTG AAGGCAGAAG
 951  CTGCAGGATG TGAAGACACG TCATGGGGTG GAATTGCGTA CTTGGCAGCT
1001  TCGTATCTCC TTTTTCTGAG ACTGAACCTG CAGAGCTAGA GTCAATGGTG
1051  CATCATATTC ATCGTCTCTC TTTTGTTTTA GACTAATCTG TAGCTAGAGT
1101  CACTGATGAA TCCTTTACAA CTTTCAAAAA AAAAA
```

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FIG. 11A

```
          1                                                  50
HP04  MLRSLLRGLT HIPRVNSAQQ PSCAHARLQF KLRSMQMTLM QPSISANLSR
HP05  MLRSLLRGLT HIPRVNSAQQ PSCAHARLQF KLRSMQLL.. ..........
ATDP7 MSVSSLFNLP .LIRLRSLA. LSSSFSSFRF AHRPLSSIS. PRKLPNFRAF
C.brew. MS.SSMLNFT .ASRIVSLPL LSSPPSRVHL PLCFFSPISL TQRFSAKLTF
ATOP5 .......... .TGPPPRFFP IRSPVPRTQL FVRAFSAV.. ..........
S.cerev. ..MTADNNSM PHGAVSSYAK LVQNQTPEDI LEEFPEIIPL QQRPN...TR

          51                                                 100
AEDRTDHMRG ASTWAGGQSQ DELMLKDECI LVDVEDNITG HASKLECHKF
SEDRTDHMRG ASTWAGGQSQ DELMLKDECI LVDVEDNITG HASKLECHKF
S..GTA.MTD TKDAGMDAVQ RRLMFEDECI LVDETDRVVG HVSKYNCHLM
SSQATT.MGE VVDAGMDAVQ RRLMFEDECI LVDENDKVVG HESKYNCHLM
.....T.MTD SNDAGMDAVQ RRLMFEDECI LVDENNRVVG HDTKYNCHLM
SSETSNDESG ETCFSGHDEE QIKLMNENCI VLDWDDNAIG AGTKKVCHLM

          101                                                150
LPHQPAGLLH RAFSVFLFDD QGRLLLQQRA RSKITFPSVW TNTCCSHPLH
LPHQPAGLLH RAFSVFLFDD QGRLLLQQRA RSKITFPSVW TNTCCSHPLH
ENIEAKNLLH RAFSVFLFNS KYELLLQQRS NTKVTFPLVW TNTCCSHPLY
ENIESENLLH RAFSVFLFNS KYELLLQQRS ATKVTFPLVW TNTCCSHPLY
EKIEAENLLH RAFSVFLFNS KYELLLQQRS KTKVTFPLVW TNTCCSHPLY
ENIE.KGLLH RAFSVFIFNE QGELLLQQRA TEKITFPDLW TNTCCSHPLC

          151                                                200
GQTPDEVDQL SQVADGTVPG AKAAAIRKLE HELGIPAHQL PA.SAFRFLT
GQTPDEVDQL SQVADGTVPG AKAAAIRKLE HELGIPAHQL PA.SAFRFLT
RE........ SELIQDNALG VRNAAQRKLL DELGIVAEDV PV.DEFTPLG
RE........ SELIDENCLG VRNAAQRKLL DELGIPAEDL PV.DQFIPLS
RE........ SELIEENVLG VRNAAQRKLF DELGIVAEDV PV.DEFTPLG
ID...DELGL KGKLDDKIKG AITAAVRKLD HELGIPEDET KTRGKFHFLN

          201                                                250
RLHYCAADVQ PAATQSALWG EHEMDYILFI ....RANVTL APNPDEVDEV
RLHYCAADVQ PAATQSALWG EHEMDYILFI ....RANVTL APNPDEVDEV
RMLY...... .KAPSDGKWG EHELDYLLFI ....VRDVKV QPNPDEVAEI
RILY...... .KAPSDGKWG EHELDYLLFI ....IRDVNL DPNPDEVAEV
RMLY...... .KAPSDGKWG EHEVDYLLFI ....VRDVKL QPNPDEVAEI
RIHY...... .MAPSNEPWG EHEIDYILFY KINAKENLTV NPNVNEVRDF
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APPROVED BY DRAFTSMAN | O.G. FIG. | CLASS | SUBCLASS

FIG. 11B

```
251                                                        300
RYVTQEELRQ MMQ....PDN GLQWSPWFRI IAARFLERWW ADLDAALNTD
RYVTQEELRQ MMQ....PDN GLQWSPWFRI IAARFLERWW ADLDAALNTD
KYVSREELKE LVKKADAGEE GLKLSPWFRL VVDNFLMKWW DHVEKGTLVE
KYMNRDDLKE LLRKADAEEE GVKLSPWFRL VVDNFLFKWW DHVEKGSLKD
KYVSREELKE LVKKADAGDE AVKLSPWFRL VVDNFLMKWW DHVEKGTITE
KWVSPNDLKT MF.....ADP SYKFTPWFKI ICENYLFNWW EQLDDLSEVE

301
KHEDWGTVHH INEA*
KHEDWGTVHH INEA*
A.IDMKTIHK L*
A.ADMKTIHK L*
A.ADMKTIHK L*
A.ADMKTIHK L*
NDRQ...IHR ML*
```

FIG. 12

```
   1  ccaaaaacaa ctcaaatctc ctccgtcgct cttactccgc catgggtgac
  51  gactccggca tggatgctgt tcagcgacgt ctcatgtttg acgatgaatg
 101  cattttggtg gatgagtgtg acaatgtggt gggacatgat accaaataca
 151  attgtcactt gatggagaag attgaaacag gtaaaatgct gcacagagca
 201  ttcagcgttt ttctattcaa ttcaaaatac gagttacttc ttcagcaacg
 251  gtctgcaacc aaggtgacat ttcctttagt atggaccaac acctgttgca
 301  gccatccact ctacagagaa tccgagcttg ttcccgaaac gcctgagaga
 351  atgctgcaca gaggaxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx
 401  xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx
 451  xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx
 501  xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx
 551  xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx
 601  xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx
 651  xxxxxxxxxx xxxxxxxxxx xxxxxxxxxx tcatgtgcaa aagggtacac
 701  tcactgaatg caatttgata tgaaaaccat acacaagctg atatagaaac
 751  acaccctcaa ccgaaaagca agcctaataa ttcgggttgg gtcgggtcta
 801  ccatcaattg ttttttttctt ttaacaactt ttaatctcta tttgagcatg
 851  ttgattcttg tcttttgtgt gtaagatttt gggtttcgtt tcagttgtaa
 901  taatgaacca ttgatggttt gcaatttcaa gttcctatcg acatgtagtg
 951  atctaaaaaa
```

FIG. 13A

```
                                                                                          70
              1
Plant beta    ..........  ...MDTLLkT PN-LaFl-p- -HG.....F- vk.-S-f-s- k---fG--K- cs--g---vc
A.t.epsilon   MECVGARNFA AMAVSTFPSW SCRRKFPVVK RYSYRNIRFG LCSVRASGGG SSGSESCVAV REDFADEXDF
Consensus     ---------- -----T---- -----F---- --------F- ---------- ---------- -E--------

                     Cyanobacterial enzyme begins ─┐
              71                                    ↓                                   140
Plant beta    Vk--SsALLa LVPETKKKNL DFELPmYDp. ...S.Kg-VV DLAvVGGGPA GLAVAQQVSE AGLSVcSIDp
A.t.epsilon   VKAGGSEIL. FVQMQQNKDM DEQSKLVDKL PPISIGDGAL DHVVIGCGPA GLALAAESAK LGLKVGLIGP
Consensus     VK---S--L- -V-------- D------D-- ---S------ D--V-G-GPA GLA-A----- -GL-V--I-P
                                                          ↑___________________________↑
          Possible subunit interaction domain              Dinucleotide-binding signature

              141                                                                       210
Plant beta    .-PKLIWPNN YGVWVDEFEA MDLLDCLDaT WSGa-VYiDd -t-KDL-RPY GRVNRKQLKS KMmQKCI-NG
A.t.epsilon   DLP...FTNN YGVWEDEFND LGLQKCIEHV WRETIVYLDD DKPITIGRAY GRVSRRLLHE ELLRRCVESG
Consensus     --P-----NN YGVW-DEF-- --L--C---- W----VY-DD -------R-Y GRV-R--L-- -----C---G

                  Conserved region #1

              211                                                                       280
Plant beta    VKFHgaKVik ViHE.E-kSm liCnDG-tIQ AtVVLDATGF SR-.LVQYDK PYnPGY.QVA YGILAEVeeH
A.t.epsilon   VSYLSSKVDS ITKASDGLRL VACDDNNVIP CRLATVASGA ASGKLLQYEV GGPRVCVQTA YGVEVEVENS
Consensus     V-----KV-- ---------- --C-D---I- ------A-G- ----L-QY-- -------Q-A YG---gv---
```

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```
                281                                                                        350
Plant beta      PFD--KMVfM DWRDsHL-NN -eLKERNs-i PTFLYAMPFS SNrIFLEETS LVARPGLmd DIQERMvARL
A.t.epsilon     PYDPDQMVFM DYRDY..TNE .KVRSLEAEY PTFLYAMPMT KSRLFFEXTC LASKDVMPFD LLKTKLMLRL
Consensus       P-D---MVFM D-RD----N- ---------- PTFLYAMP-- --R-F-EXT- L--------D --------RL

                Conserved region #2                 Conserved region #3

                351                                                                        420
Plant beta      -HLGIkVKsI EEDEhCvIPM GGpLPVlPQR VVGiGGTAGm VHPSTGYMVA RTLAAAPvVA NAIi-YLgSe
A.t.epsilon     DTLGTRILKT YEEEWSVIPV GGSLPNTEQK NLAFGAAASM VHPATGYSVV RSLSEAPKYA SVIAEILREE
Consensus       --LGI----- -E-E---IP- GG-LP---Q- ----G--A-M VHP-TGY-V- R-L--AP--A --I---L--E

                                          Conserved region #4       Predicted TM helix

                421                                                              480
Plant beta      -s-s..G-eL SaeVWkDLWP IERRRQREFF CFGMDILLKL DLpATRRFFD AFFDLaPrYW
A.t.epsilon     TTKQINSN.I SRQAWDTLWP PERKRQRAFF LFGLALIVQF DTEGIRSFFR TFFRLPKWMW
Consensus       ---------- S---W--LWP -ER-RQR-FF -FG------- D----R-FF- -FF-L----W

                             Conserved region #5

                481                                                   533
Plant beta      HGFLSSRLfL PELivFGLSL FShASNTSR- EIMTK.GT-P Lv-MINNLlQ D--
A.t.epsilon     QGFLGSTLTS GDLVLFALYM FVISPNNLRK GLINHLISDP TGATMIKTYL KV.
Consensus       -GFL-S-L-- --L--F-L-- F----N--R- ---------- ---------- ---

                Predicted TM helix
```

FIG. 13B

FIG. 14A

Adonis palaestina ε-cyclase cDNA #5 Length: 1898

```
   1  aaaggagtgt tctattaatg ttactgtcgc attcttgcaa cacttatatt
  51  caaactccat tttcttcttt tctcttcaaa acaacaaact aatgtgagca
 101  gagtatctgg ctatggaact acttggtgtt cgcaacctca tctcttcttg
 151  ccctgtgtgg acttttggaa caagaaacct tagtagttca aaactagctt
 201  ataacataca tcgatatggt tcttcttgta gagtagattt tcaagtgaga
 251  gctgatggtg gaagcgggag tagaagttct gttgcttata aagagggttt
 301  tgtggatgaa gaggatttta tcaaagctgg tggttctgag cttttgtttg
 351  tccaaatgca gcaaacaaag tctatggaga aacaggccaa gctcgccgat
 401  aagttgccac caatacctttt tggagaatcc gtgatggact tggttgtaat
 451  aggttgtgga cctgctggtc tttcactggc tgcagaagct gctaagctag
 501  ggttgaaagt tggccttatt ggtcctgatc ttccttttac aaataattat
 551  ggtgtgtggg aagacgagtt caaagatctt ggacttgaac gttgtatcga
 601  gcatgcttgg aaggacacca tcgtatatct tgataatgat gctcctgtcc
 651  ttattggtcg tgcatatgga cgagttagtc gacatttgct acatgaggag
 701  ttgctgaaaa ggtgtgtgga gtcaggtgta tcatatctgg attctaaagt
 751  ggaaaggatc actgaagctg gtgatggcca tagccttgta gtttgtgaaa
 801  atgagatctt tatcccttgc aggcttgcta ctgttgcatc tggagcagct
 851  tcagggaaac ttttggagta tgaagtaggt ggccctcgtg tttgtgtcca
 901  aaccgcttat ggggtggagg ttgaggtgga gaacaatcca tacgatccca
 951  acttaatggt attcatggac tacagagact atatgcaaca gaaattacag
1001  tgctcggaag aagaatatcc aacatttctC tatgtcatgc ccatgtcgcc
1051  aacaagactt ttttttgagg aaacctgttt ggcctcaaaa gatgccatgc
1101  cattcgatct actgaagaga aaactgatgt cacgattgaa gactctgggt
1151  atccaagtta caaaagttta tgaagaggaa tggtcatata ttcctgttgg
1201  tggttcttta ccaaacacag agcaaaagaa cctagcattt ggtgctgcag
1251  caagcatggt gcatccagca acaggctatt cggttgtacg gtcactgtca
1301  gaagctccaa aatatgcttc tgtaattgca aagattttga agcaagataa
1351  ctctgcgtat gtggtttctg gacaaagtag tgcagtaaac atttcaatgc
1401  aagcatggag cagtctttgg ccaaaggagc gaaaacgtca aagagcatTc
1451  tttcttttTg gattagagct tattgtgcag ctagatattg aagcaaccag
1501  aacattcttt agaaccttct tccgcttgcc aacttggatg tggtggggtt
1551  tccttgggtc ttcactatca tctttcgatc tcgtcttgtt ttccatgtac
1601  atgtttgttt tggcgccaaa cagcatgagg atgtcacttg tgagacattt
1651  gctttcagat ccttctggtg cagttatggt aagagcttac ctcgaaaggt
1701  agtctcatct attattaaac tctagtgttt caccaaataa atgaggatcc
1751  ttcgaatgtg tatatgatca tctctatgta tatcctgtac tctaatctca
1801  taaagtaaat gccgggtttg atattgttgt gtcaaaccgg ccaatgatat
1851  aaagtaaatt tattgataca aaagtagttt ttttccttaa aaaaaaaa
```

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FIG. 14B

Adonis palaestina ε-cyclase #5 predicted polypeptide
TRANSLATE from: 113 to: 1702 Length: 529 amino acids

```
  1  MELLGVRNLI SSCPVWTFGT RNLSSSKLAY NIHRYGSSCR VDFQVRADGG
 51  SGSRSSVAYK EGFVDEEDFI KAGGSELLFV QMQQTKSMEK QAKLADKLPP
101  IPFGESVMDL VVIGCGPAGL SLAAEAAKLG LKVGLIGPDL PFTNNYGVWE
151  DEFKDLGLER CIEHAWKDTI VYLDNDAPVL IGRAYGRVSR HLLHEELLKR
201  CVESGVSYLD SKVERITEAG DGHSLVVCEN EIFIPCRLAT VASGAASGKL
251  LEYEVGGPRV CVQTAYGVEV EVENNPYDPN LMVFMDYRDY MQQKLQCSEE
301  EYPTFLYVMP MSPTRLFFEE TCLASKDAMP FDLLKRKLMS RLKTLGIQVT
351  KVYEEEWSYI PVGGSLPNTE QKNLAFGAAA SMVHPATGYS VVRSLSEAPK
401  YASVIAKILK QDNSAYVVSG QSSAVNISMQ AWSSLWPKER KRQRAFFLFG
451  LELIVQLDIE ATRTFFRTFF RLPTWMWWGF LGSSLSSFDL VLFSMYMFVL
501  APNSMRMSLV RHLLSDPSGA VMVRAYLER*
```

FIG. 15A

DNA sequence of potato cDNA (GenBank R27545) obtained from Nicholas J. Provart

```
potato.seq  Length: 1378  August 2, 1996  13:06  Type: N  Check: 605  ..
   1  tagcggnnnn naggatgagt tcaaagatct tggtcttcaa gcctgcattg
  51  aacatgtttg gcgggatacc attgtatatc ttgatgatga tgatcctatt
 101  cttattggcc gtgcctatgg aagagttagt cgccatttac tgcacgagga
 151  gttactcaaa aggtgtgtgg aggcaggtgt tttgtatcta aactcgaaag
 201  tggataggat tgttgaggcc acaaatggcc acagtcttgt agagtgcgag
 251  ggtgatgttg tgattccctg caggtttgtg actgttgcat cgggagcagc
 301  ctcggggaaa ttcttgcagt atgagttggg aggtcctaga gtttctgttc
 351  aaacagctta tggagtggaa gttgaggtcg ataacaatcc atttgacccg
 401  agcctgatgg ttttcatgga ttatagagac tatgtcagac acgacgctca
 451  atctttagaa gctaaatatc caacatttct ctatgccatg cccatgtctc
 501  caacacgagt ctttttcgag gaaacttgtt tggcttcaaa agatgcaatg
 551  ccattcgatc tgttaaagaa aaaattgatg ttacgattga acaccctcgg
 601  tgtaagaatt aaagaaattt atgaggagga atggtcttac ataccagttg
 651  gaggatcttt gccaaataca gaacaaaaaa cacttgcatt tggtgctgct
 701  gctagcatgg ttcatccagc cacaggttat tcagtcgtca gatcactgtc
 751  tgaagctcca aaatgcgcct tcgtgcttgc aaatatatta cgacaaaatc
 801  atagcaagaa tatgcttact agttcaagta ccccgagtat ttcaactcaa
 851  gcttggaaca ctctttggcc acaagaacga aaacgacaaa gatcgttttt
 901  cctatttgga ctggctctga tattgcagct ggatattgag gggataaggt
 951  catttttccg cgcgttcttc cgtgtgccaa aatggatgtg gcagggattt
1001  cttggttcaa gtctttcttn agcagacctc atgttatttg ccttctacat
1051  gtttattatt gcaccaaatg acatgagaag aggcttaatc agacatcttt
1101  tatctgatcc tactggtgca acattgataa gaacttatct tacattttag
1151  agtaaattcc tcctacaata gttgttgaan nagaggcctc attacttcag
1201  attcataaca gaaatcgcgg tctctcgagg ccttgtatat aacattttca
1251  ctaggttaat attgcttgaa taagttgcac agtttcagtt tttgtatctg
1301  cttctttttt gtccaagatc atgtattgan ccaatttata tacattgcca
1351  gtatatataa attttataaa aaaaaaaa

poteps.pep  Length: 378  TRANSLATE from: 14  to: 1147
   1  DEFKDLGLQA CIEHVWRDTI VYLDDDDPIL IGRAYGRVSR HLLHEELLKR
  51  CVEAGVLYLN SKVDRIVEAT NGHSLVECEG DVVIPCRFVT VASGAASGKF
 101  LQYELGGPRV SVQTAYGVEV EVDNNPFDPS LMVFMDYRDY VRHDAQSLEA
 151  KYPTFLYAMP MSPTRVFFEE TCLASKDAMP FDLLKKKLML RLNTLGVRIK
 201  EIYEEEWSYI PYGGSLPNTE QKTLAFGAAA SMVHPATGYS VVRSLSEAPK
 251  CAFVLANILR QNHSKNMLTS SSTPSISTQA WNTLWPQERK RQRSFFLFGL
 301  ALILQLDIEG IRSFFRAFFR VPKWMWQGFL GSSLSXADLM LFAFYMFIIA
 351  PNDMRRGLIR HLLSDPTGAT LIRTYLTF*
```

FIG. 15B

Chimeric lettuce/potato lycopene ε-cyclase: converts lycopene to δ-carotene, the lettuce cDNA converts lycopene to ε-carotene and the potato cDNA does not produce an active enzyme

(amino acids in lower case are from lettuce and those in uppercase are from the potato cDNA; an *AvaII* site in common to the two cDNAs was used to construct the chimera)

```
  1 mecfgarnmt atmavftcpt ftdcnirhkf sllkqrrftn lsassslrqi
 51 kcsaksdrcv vdkqgisvac eedyvkaggs elffvqmqrt ksmesqskls
101 eklaqipign cildlvvigc gpaglalaae saklglnvgl igpdlpftnn
151 ygvwqdefig lglegciehs wkdtlvyldd adpirigray grvhrdllhe
201 ellrrcvesg vsylsskver iteapngysl iecegnitip crlatvasga
251 asgkfleyel gGPRVSVQTA YGVEVEVDNN PFDPSLMVFM DYRDYVRHDA
301 QSLEAKYPTF LYAMPMSPTR VFFEETCLAS KDAMPFDLLK KKLMLRLNTL
351 GVRIKEIYEE EWSYIPVGGS LPNTEQKTLA FGAAAASMVHP ATGYSVVRSL
401 SEAPKCAFVL ANILRQNHSK NMLTSSSTPS ISTQAWNTLW PQERKRQRSF
451 FLFGLALILQ LDIEGIRSFF RAFFRVPKWM WQGFLGSSLS XADLMLFAFY
501 MFIIAPNDMR RGLIRHLLSD PTGATLIRTY LTF*
```

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FIG. 16

GAP comparison of Arabidopsis ε-cyclase x potato ε-cyclase (partial)

blosum62.cmp	Gap Weight: 12	Average Match:	2.912
	Length Weight: 4	Average Mismatch:	-2.003
	Quality: 1485	Length:	529
	Ratio: 3.929	Gaps:	1
	Percent Similarity: 79.893	Percent Identity:	76.139

Match display thresholds for the alignment(s):
| = IDENTITY : = 2 . = 1

```
151  EDEFNDLGLQKCIEHVWRETIVYLDDDKPITIGRAYGRVSRRLLHEELLR 200
     ||| ||||| |||||||:||||||||  || ||||||||||  |||||||:
   1  .DEFKDLGLQACIEHVWRDTIVYLDDDDPILIGRAYGRVSRHLLHEELLK 49

201  RCVESGVSYLSSKVDSITEASDGLRLVACDDNNVIPCRLATVASGAASGK 250
     ||||.|| ||.|||| | ||..|  || |: . |||||  ||||||||||
    50  RCVEAGVLYLNSKVDRIVEATNGHSLVECEGDVVIPCRFVTVASGAASGK 99

251  LLQYEVGGPRVCVQTAYGVEVEVENSPYDPDQMVFMDYRDYTNEKVRSLE 300
     ||||.|||||  ||||||||||:|.|:||  |||||||||      .|||
    100  FLQYELGGPRVSVQTAYGVEVEVDNNPFDPSLMVEMDYRDYVRHDAQSLE 149

301  AEYPTFLYAMPMTKSRLFFEETCLASKDVMPFDLLKTKLMLRLDTLGIRI 350
     |.||||||||||. .|.|||||||||| ||||||| ||||||.|||:||
    150  AKYPTFLYAMPMSPTRVFFEETCLASKDAMPFDLLKKKLMLRLNTLGVRI 199

351  LKTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAP 400
     . ||||||||||||||||||| |||||||||||||||||||||||||||
    200  KEIYEEEWSYIPVGGSLPNTEQKTLAFGAAASMVHPATGYSVVRSLSEAP 249

401  KYASVIAEILREETTKQI.....NSNISRQAWDTLWPPERKRQRAFFLFG 445
     | | |:| |||:  .| .       .|| |||.|||| ||||||.|||||
    250  KCAFVLANILRQNHSKNMLTSSSTPSISTQAWNTLWPQERKRQRSFFLFG 299

446  LALIVQFDTEGIRSFFRTFFRLPKWMWQGFLGSTLTSGDLVLFALYMFVI 495
     ||||.| | |||||||| |||.||||||||||.|.  ||.||| |||:|
    300  LALILQLDIEGIRSFFRAFFRVPKWMWQGFLGSSLSXADLMLFAFYMFII 349

496  SPNNLRKGLINHLISDPTGATMIKTYLKV 524
     .||.:|:||| ||:||||||:|:|||
    350  APNDMRRGLIRHLLSDPTGATLIRTYLTF 378
```

FIG. 17A

Adonis palaestina Ipil

```
   1  attcatcttc agcagcgctg tcgtactctt tctatatctt cttccatcac
  51  taacagtagt cgccgacggt tgaatcggct attcgcctca acgtcaacta
 101  tgggtgaagt cactgatgct ggaatggatg ctgttcagaa gcggctcatg
 151  ttcgacgacg aatgtatttt ggtggatgag aatgacaagg tcgtcgggca
 201  tgattccaaa tacaactgtc atttgatgga aaagatagag gcagaaaatt
 251  tgcttcacag agccttcagt gttttcttgt tcaactcaaa atatgaattg
 301  cttcttcagc aacgatccgc cacaaaggta acattcccgc tcgtatggac
 351  aaacacatgt tgcagtcatc ctctctttcg tgattccgag ctcatagaag
 401  aaaattatct cggtgtacga aacgctgcac aaagaaagct tttagacgag
 451  ctaggcattc cagctgaaga tgtcccagtt gatgaattta ctcctcttgg
 501  tcgcattctt tacaaagctc catctgacgg caaatgggga gagcacgaat
 551  tggactatct cctatttatt gtccgagatg tgaaatacga tccaaaccca
 601  gatgaagttg ctgatgctaa gtatgttaat cgcgaggagt tgagagagat
 651  actgagaaaa gctgatgctg gtgaagaggg actcaagttg tctccttggt
 701  ttagattggt tgttgataac tttttgttca agtggtggga tcatgtagag
 751  cagggtacga ttaaggaagt tgctgacatg aaaactatcc acaagttgac
 801  ttaagaggac ttctctcctc tgttctacta tttgtttttt gctacaataa
 851  gtgggtggtg ataagcagtt tttctgtttt ctttaattta tggcttttga
 901  atttgcctcg atgttgaact tgtaacatat ttagacaaat atgagacctt
 951  gtaagttgaa tttgaggctg aatttatatt tttgggaaca taataatgtt
1001  aa
```

FIG. 17B

Adonis palaestina Ipi2

```
   1  ttttaaagct ctttcgctcc accaccatca aagccagcca aatttctctg
  51  tacaaaagtt aaaaacaccg ctttgggctt tggcccctcc atatcggaat
 101  ccttgtttac gatacgcatc taaaccagta attctcggtt ttaatttgtt
 151  tcctaaatta ggcccctttc cggaatcccg agaattatgt cgtcgatcag
 201  gattaatcct ttatatagta tcttctccac caccactaaa acattatcag
 251  cttcgtgttc ttctcccgct gttcatcttc agcagcgttg tcgtactctt
 301  tctatttctt cttccatcac taacagtcct cgccgagggt tgaatcggct
 351  gttcgcctca acgtcgacta tgggtgaagt cgctgatgct ggtatggatg
 401  ccgtccagaa gcggcttatg ttcgacgatg aatgtatttt ggtggatgag
 451  aatgacaagg tcgtcggaca tgattccaaa tacaactgtc atttgatgga
 501  aaagatagag gcagaaaact tgcttcacag agccttcagt gttttcttat
 551  tcaactcaaa atacgagttg cttcttcagc aacgatctgc aacgaaggta
 601  acattcccgc tcgtatggac aaacacctgt tgcagccatc ccctcttccg
 651  tgattccgaa ctcatagaag aaaattttct cggggtacga aacgctgcac
 701  aaaggaagct tttagacgag ctaggcattc cagctgaaga cgtaccagtt
 751  gatgaattca ctcctcttgg tcgcattctt tacaaagctc catctgacgg
 801  aaaatgggga gagcacgaac tggactatct tctgtttatt gtccgagatg
 851  tgaaatacga tccaaaccca gatgaagttg ctgacgctaa gtacgttaat
 901  cgcgaggagt tgaaagagat actgagaaaa gctgatgcag gtgaagaggg
 951  aataaagttg tctccttggt ttagattggt tgtggataac tttttgttca
1001  agtggtggga tcatgtagag gaggggaaga ttaaggacgt cgccgacatg
1051  aaaactatcc acaagttgac ttaagagaaa gtctcttaag ttctactatt
1101  tggtttttgc ttcaataagt ggatggtgat gagcagtttt tatgcttcct
1151  ttaattttgg cttttcaatt tgctttatgt gttgaacttg taacatattt
1201  agtcaaatat gagaccttgt gagttgaatt tgaggttata tttatagttt
1251  tgggaacata aaaaaaaaaa
```

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FIG. 18A

Haematococcus pluvialis Ipil

```
   1 ctcggtagct ggccacaatc gctatttgga acctggcccg gcggcagtcc
  51 gatgccgcga tgcttcgttc gttgctcaga ggcctcacgc atatcccccg
 101 cgtgaactcc gcccagcagc ccagctgtgc acacgcgcga ctccagttta
 151 agctcaggag catgcagatg acgctcatgc agcccagcat ctcagccaat
 201 ctgtcgcgcg ccgaggaccg cacagaccac atgaggggtg caagcacctg
 251 ggcaggcggg cagtcgcagg atgagctgat gctgaaggac gagtgcatct
 301 tggtggatgt tgaggacaac atcacaggcc atgccagcaa gctggagtgt
 351 cacaagttcc taccacatca gcctgcaggc ctgctgcacc gggccttctc
 401 tgtgttcctg tttgacgatc aggggcgact gctgctgcaa cagcgtgcac
 451 gctcaaaaat caccttccca agtgtgtgga cgaacacctg ctgcagccac
 501 cctttacatg ggcagacccc agatgaggtg gaccaactaa gccaggtggc
 551 cgacggaaca gtacctggcg caaaggctgc tgccatccgc aagttggagc
 601 acgagctggg gataccagcg caccagctgc cggcaagcgc gtttcgcttc
 651 ctcacgcgtt tgcactactg tgccgcggac gtgcagccag ctgcgacaca
 701 atcagcgctc tggggcgagc acgaaatgga ctacatcttg ttcatccggg
 751 ccaacgtcac cttggcgccc aaccctgacg aggtggacga agtcaggtac
 801 gtgacgcaag aggagctgcg gcagatgatg cagccggaca acgggctgca
 851 atggtcgccg tggtttcgca tcatcgccgc gcgcttcctt gagcgttggt
 901 gggctgacct ggacgcggcc ctaaacactg acaaacacga ggattgggga
 951 acggtgcatc acatcaacga agcgtgaaag cagaagctgc aggatgtgaa
1001 gacacgtcat ggggtggaat tgcgtacttg gcagcttcgt atctcctttt
1051 tctgagactg aacctgcagt caggtcccac aaggtcaggt aaaatggctc
1101 gataaaatgt accgtcactt tttgtcgcgt atactgaact ccaagaggtc
1151 aaaaaaaaaa aaaaa
```

FIG. 18B

Haematococcus pluvialis Ipi2

```
   1  tggaacctgg cccggcggca gtccgatgcc gcgatgcttc gttcgttgct
  51  cagaggcctc acgcatatcc cgcgcgtgaa ctccgcccag cagcccagct
 101  gtgcacacgc gcgactccag tttaagctca ggagcatgca gctgcttgcc
 151  gaggaccgca cagaccacat gaggggtgca agcacctggg caggcgggca
 201  gtcgcaggat gagctgatgc tgaaggacga gtgcatctta gtggatgctg
 251  acgacaacat cacaggccat gccagcaagc tggagtgcca caaattccta
 301  ccacatcagc ctgcaggcct gctgcaccgg gccttctctg tgttcctgtt
 351  tgacgaccag gggcgactgc tgctgcaaca gcgtgcacgc tcaaaaatca
 401  ccttcccaag tgtgtggacg aacacctgct gcagccaccc tctacatggg
 451  cagaccccag atgaggtgga ccaactaagc caggtggccg acggcacagt
 501  acctggcgca aaagctgctg ccatccgcaa gttggagcac gagctgggga
 551  taccagcgca ccagctgccg gcaagcgcgt ttcgcttcct cacgcgtttg
 601  cactactgtg ccgcggacgt gcagccggct gcgacacaat cagcgctctg
 651  gggcgagcac gagatggact acatcttatt catccgggcc aacgtcacct
 701  tggcgcccaa ccctgacgag gtggacgaag tcaggtacgt gacgcaagag
 751  gagctgcggc agatgatgca gccggacaac gggttgcaat ggtcgccgtg
 801  gtttcgcatc atcgccgcgc gcttccttga gcgttggtgg gctgacctgg
 851  acgcggccct aaacactgac aaacacgagg attggggaac ggtgcatcac
 901  atcaacgaag cgtgaaggca gaagctgcag gatgtgaaga cacgtcatgg
 951  ggtggaattg cgtacttggc agcttcgtat ctccttttc tgagactgaa
1001  cctgcagagc tagagtcaat ggtgcatcat attcatcgtc tctcttttgt
1051  tttagactaa tctgtagcta gagtcactga tgaatccttt acaactttca
1101  aaaaaaaaa
```

FIG. 19A

Lactuca sativa Ipi1

```
   1  tgccaaaatg ttgaaatttc ccccttttaa aaccattgct accatgatct
  51  cttctccata ttcttccttc ttgctgcctc ggaaatcttc tttccctcca
 101  atgccgtctc tcgcagccgc tagtgttttc ctccaccctc tttcgtctgc
 151  cgctatgggc gattccagca tggatgctgt ccagcgacgt ctcatgttcg
 201  atgacgaatg cattttggtg gatgagaatg acaaagtggt tggccatgat
 251  actaaataca attgtcattt gatggagaag attgaaaagg gaaatatgct
 301  acacagagca ttcagtgtgt tcttgttcaa ctcgaaatat gaattactcc
 351  ttcagcaacg ttctgcaacc aaggtgactt tccctttggt atggacaaac
 401  acgtgttgca gccatccact atacagggag agtgagctta ttgacgaaaa
 451  cgcccttggg gtgaggaatg ctgcacagag gaagctcctg gatgaactcg
 501  gcatccctgg agcagatgtt ccggttgatg agttcactcc attgggtcgc
 551  attctataca aggccgcatc ggatggaaag tggggagaac atgaacttga
 601  ttacctgctg tttatggtac gtgatgttgg tttggatccg aacccagatg
 651  aagtgaaaga tgtaaaatat gtgaaccggg aagagctgaa ggaattggta
 701  aggaaggcgg atgctggtga agagggtgtg aagctgtccc cgtggttcaa
 751  attgattgtc gataatttct tgtttcagtg gtgggatcga ctccataagg
 801  gaaccctaac cgaagctatt gatatgaaaa caatccacaa actcacataa
 851  aaacactaca ctagtaggag agaggattat atgagatatt tgttatatgt
 901  gaaattgaaa ttcagatgaa tgcttgtatt tatttctatt tggacaaact
 951  tcaacttctt tttgctacct tatcagaaaa aaaaa
```

FIG. 19B

Lactuca sativa Ipi2

```
   1  tattcgcttc aaaatctctt ccattaactg ctcaaatctc caccttcgcc
  51  ggtcttaatc tccgccggcg cactttcacc accataaccg ccgccatggg
 101  tgacgattcc ggcatggacg ctgtccagag acgtctcatg tttgatgatg
 151  aatgcatttt ggttgatgaa aatgacaatg ttcttgggca tgataccaaa
 201  tacaattgtc acttgatgga gaagattgag aaagataatt tgcttcatag
 251  agcattcagt gtatttttat tcaattcaaa atacgaatta ctccttcagc
 301  aaaggtcaga aaccaaggtg acatttcctt tggtatggac aaacacctgt
 351  tgcagccatc cactatacag agaatcggag ttaattcccg aaaatgccct
 401  tggggtcaga aatgctgcac agaggaagct tctagatgaa ctcggtatcc
 451  ctgctgaaga tgttccagtt gatgagttca caactttagg tcgcatgttg
 501  tacaaggctc catctgatgg aaaatggggt gaacatgaag ttgattacct
 551  actcttcctc gtgcgtgacg ttgccgtgaa cccaaaccct gatgaggtgg
 601  cggacattag atacgtgaac caagaagagt taaaagagtt actaaggaag
 651  gcggatgcgg gtgaggaggg tttgaaattg tccccatggt ttaggctagt
 701  ggtggacaac ttcttgttca aatggtggga tcatgtccaa aaggggacac
 751  tcaatgaagc aattgacatg aaaaccattc ataagttgat atgaaaaatg
 801  gttaatattt atggtggtgg tttggagcta ataatttgtg tgttcaagtc
 851  tcggtccttc ttttttaac gttttttttt tttctttat tgggagtgtt
 901  tattgtgtac ttgtaacgta ggccctttgg ttacgcttta agagtttaat
 951  aaagaaccac cgttaattta aaaaaaaaaa aaaaaaaa
```

FIG. 20

Chlamydomonas reinhardtii Ipi1

(Note: the isomerase cDNA probably ends at ca. base 1103; the second half of the cDNA is similar to extensin and other hydroxyproline-rich structural proteins)

```
   1 ggcacgagct cgagtttgtt ttaccatgac atcgggaatt tggaagcttg
  51 aactacctca attactcaag taactcgcgg caacacattt cgcgcgccat
 101 cgctgttttc tctgctccag ctaccgagca gcattgcttt agatcgcttt
 151 gatgtcataa actcccactt atatgagatc cagtttcatc gagcccaagc
 201 ccagagcgca acctgtctta agccgcggca gggcgtccat gcgcctcgcg
 251 caaagccgtg ctctcgttgc gcgtgtcagc tccgccctgt ggccgggagc
 301 aggactttca caggctcaaa gcgttgcggt gcgaatggcg agttcgtcaa
 351 cctgggaagg cacgggcctg agccaggatg acttcatgca gcgggacgag
 401 tgcttggtgg tggacgagca ggaccggctg ctaggcaccg ccaacaagta
 451 cgactgccac cgcttcgagg cggccaaggg ccagccctgc ggccgcctgc
 501 accgcgcctt ctccgtgttc ctgttcagcc ccgacggccg actgctgctg
 551 cagcagcgcg cagccagcaa ggtgacgttc ccgggtgtgt ggaccaacac
 601 ctgctgctcg cacccgctgg cgggccaggc gccggacgag gtggacctgc
 651 cggcggcggt agcctcgggc caggtgccgg gcatcaaggc ggcggcggtg
 701 cgcaagctgc agcacgagct ggggataccg ccggagcagg ttcccgcctc
 751 ctccttctcc ttcctcacgc gtctgcacta ctgcgccgcc gacaccgcca
 801 cgcacggccc ggcggcggag tggggcgagc acgaggtgga ctacgtgctg
 851 ttcgtgcggc cgcagcagcc cgtcagcctg cagcccaacc cagacgaggt
 901 ggacgccacg cgctacgtga cgctgccgga gcttcagtcc atgatggcgg
 951 accccggcct cagctggagc ccctggttcc gcatcctggc cacacagccc
1001 gccttcctgc ccgcctggtg gggcgacctg aagcggcgct ggcgcccggg
1051 cggcagccga ctgtaggact ggggcaccat ccaccgcgtc atgtgaagaa
1101 aaaggggaag caggggcggg agcgggggat gaatgggaat gtgaatgcga
1151 ttgtgatgcg gcgtgggatg aggtctgaag acaggggggaa aatcgggggg
1201 cgggcgtgag cgtgtgtgta cgtgagcgac aaagccggga ggcggaccgc
1251 gcgatgggta catgtgtgtg cggagggtcg gtgggtcggt cggttgcgcg
1301 gcatagcgtg ttgtgtgtgt gcggctgcgc gggtatgtgg gcacccgggc
1351 acggaggaga aggcacacgc aggtggcgcg gaggtgtgtc aggggccatg
1401 ggcgggcctc actcctggtc gtgcccagtg gtctcgtggg cagagtggca
1451 ggggctgcac ccatatgagc ggcgcactgc cgcgctgggc taagtcctta
1501 tcacttggtg aggtggggcg aggtggctgt gggcggcggg cgcagtggca
1551 gaaggacacg gtgtgtgagc ggtggagctc tggccgtgcc ggccgtgagg
1601 ggcggatagc gatatgacgt tgtgcttggc cgctgtaatg cgggagaatg
1651 tgcaggccgc gagaagcggg cggtggcagg aggccgcagg ctgcagcacc
1701 cgttggggag gtgccgcctg caggcgcggc gccgggcggg cctgagtaat
1751 gggcgcctga gtagtggcgg ccacaggagg cgcaggaggc agcagcagga
1801 ggacgagctg gagggacccg ttggcaaccc aaggttgcgc gtgtaacata
1851 gtggccatac aaaaaaaaaa aaaa
```

FIG. 21A

Tagetes erecta Ipil

```
   1  ccaaaaacaa ctcaaatctc ctccgtcgct cttactccgc catgggtgac
  51  gactccggca tggatgctgt tcagcgacgt ctcatgtttg acgatgaatg
 101  cattttggtg gatgagtgtg acaatgtggt gggacatgat accaaataca
 151  attgtcactt gatggagaag attgaaacag gtaaaatgct gcacagagca
 201  ttcagcgttt ttctattcaa ttcaaaatac gagttacttc ttcagcaacg
 251  gtctgcaacc aaggtgacat ttcctttagt atggaccaac acctgttgca
 301  gccatccact ctacagagaa tccgagcttg ttcccgaaaa cgcccttgga
 351  gtaagaaatg ctgcacagag gaagctgttg gatgaactcg gtatccctgc
 401  tgaagatgtt cccgttgatc agtttactcc tttaggtcgc atgctctaca
 451  aggctccatc tgatggaaag tggggagaac atgaacttga ctacctactt
 501  ttcatagtga gagacgttgc tgtaaacccg aacccagatg aagtggcgga
 551  tatcaaatat gtganccang aagagttaaa ggagctgcta aggaaagcag
 601  atgcggggga ggagggtttg aagctgtctc catggttcag gttagtggtt
 651  gataacttct tgttcaagtg gtgggatcat gtgcaaaagg gtacactcac
 701  tgaagcaatt gatatgaaaa ccatacacaa gctgatatag aaacacaccc
 751  tcaaccgaaa agttcaagcc taataattcg ggttgggtcg ggtctaccat
 801  caattgtttt tttcttttaa gaagttttaa tctctatttg agcatgttga
 851  ttcttgtctt ttgtgtgtaa gattttgggt ttcgtttcag ttgtaataat
 901  gaaccattga tggtttgcaa tttcaagttc ctatcgacat gtagtgatct
 951  aaaaaa
```

FIG. 21B

Oryza sativa Ipil

```
   1  cctccctttg cctcgcgcag aggcggccgc gccttctccg ccgcgaggat
  51  ggccggcgcc gccgccgccg tggaggacgc cgggatggac gaggtccaga
 101  agcggctcat gttcgacgac gaatgcattt tggtggatga acaagacaat
 151  gttgttggcc atgaatcaaa atataactgc catctgatgg aaaaaatcga
 201  atctgaaaat ctacttcata gggctttcag tgtattcctg ttcaactcaa
 251  aatatgaact cctactccag caacgatctg caacaaaggt tacatttcct
 301  ctagtttgga ccaacacttg ctgcagccat cctctgtacc gtgagtctga
 351  gcttatacag gaaaactacc ttggtgttag aaatgctgct cagaggaagc
 401  tcttggatga gctgggcatc ccagctgaag atgtgccagt tgaccaattc
 451  acccctcttg gtcggatgct ttacaaggcc ccatctgatg gaaaatgggg
 501  tgaacacgag cttgactacc tgctgttcat cgtccgcgac gtgaaggtag
 551  tcccgaaccc ggacgaagtg gccgatgtga aatacgtgag ccgtgagcag
 601  ctgaaggagc tcatccgcaa agcggacgcc ggagaggaag gcctgaagct
 651  gtctccctgg ttccggctgg ttgttgacaa cttcctcatg ggctggtggg
 701  atcacgtcga gaaaggcacc ctcaacgagg ccgtggacat ggagaccatc
 751  cacaagctga agtaaggact gcgatgttgt ggctggaaag aatgatcctg
 801  aagactctgt tcttgtgctg ctgcatatta ctcttaccag ggaagttgca
 851  gaagtcagaa gaagcttttg tatgtttctg ggtttggagc ttggaagtgt
 901  tgggctctgc tgactgagag attcccttat agagtgtcta tgttaattta
 951  gcaaacttct atattataca tgattagtta attgttcggt gtctgaataa
1001  agaacaatag catgttccat gtttatttgc t
```

09/701395

APPROVED BY DRAFTSMAN | O.G. | CLASS | SUBCLASS

ClustalW 1.7 Multiple Sequence Alignment of Plant and Green Algal Isopentenyl Pyrophosphate Isomerases (IPI)

These amino acid sequences were predicted by cDNAs that were isolated and identified by color complemtation in *E.coli*

	1	15 16	30 31	45 46	60 61	75 76 90	
1 *T.erecta* 1	---------------	---------------	---------------	---------------	-MGD--DSGMDAVQR	RLMFDDECILVDECD	27
2 *L.sativa* 1	--------MLKFPPF	KTIATMISSPYSSFL	LPRKSSFPPMPS---	-LAAASVFLHPLSSA	AMGD--SS-MDAVQR	RLMFDDECILVDEND	75
3 *L.sativa* 2	---------------	---------------	---------------	---------------	-MGD--DSGMDAVQR	RLMFDDECILVDEND	27
4 *A.palaestina* 2	MSSIRINPLYSIFST	TTKTLSASCSSPAVH	LQQRCRTLSISSSIT	NSPRRGLNRLFASTS	TMGEVADAGMDAVQK	RLMFDDECILVDEND	90
5 *A.palaestina* 1	---------------	---------------	---------------	---------------	-MGEVTDAGMDAVQK	RLMFDDECILVDEND	29
6 *O.sativa* 1	---------------	---------------	---------------	------------MAG	AAAAVEDAGMDEVQK	RLMFDDECILVDEQD	33
7 *A.thaliana* 1	---MSVSSLFNLPLI	RLRSLALSSSFSSFR	FAHRP--LSSIS---	--PRKLPNFRAFSGT	AMTDTKDAGMDAVQR	RLMFEDECILVDETD	80
8 *A.thaliana* 2	---------------	---------------	---------------	---------------	-MTDSNDAGMDAVQR	RLMFEDECILVDENN	29
9 *H.pluvialis* 1	---MLRSLLRGLTHI	PRVNSAQQPSCAHAR	LQFKLRSMQLLS---	---------EDRTDH	MRGASTWAG-GQSQD	ELMLKDECILVDVED	74
10 *H.pluvialis* 2	---MLRSLLRGLTHI	PRVNSAQQPSCAHAR	LQFKLRSMQMTLMQP	SISANLSRAEDRTDH	MRGASTWAG-GQSQD	ELMLKDECILVDVED	86
11 *C.reinhardtii* 1	---MRSSFIE---PK	PRAQPVLSRGRASMR	LAQSRALVARVSSAL	WPGAGLSQAQSVAVR	MASSSTWEGTGLSQD	DFMQRDECLVVDEQD	84

	91 105	106 120	121 135	136 150	151 165	166 180	
1 *T.erecta* 1	NVVGHDTKYNCHLME	KIE--TGKMLHRAFS	VFLENSKYELLLQQR	SATKVTFPLVWTNTC	CSHPLYRES------	--ELVPENALGVRNA	107
2 *L.sativa* 1	KVVGHDTKYNCHLME	KIE--KGNMLHRAFS	VFLENSKYELLLQQR	SATKVTFPLVWTNTC	CSHPLYRES------	--ELIDENALGVRNA	155
3 *L.sativa* 2	NVLGHDTKYNCHLME	KIE--KDNLLHRAFS	VFLFNSKYELLLQQR	SETKVTFPLVWTNTC	CSHPLYRES------	--ELIPENALGVRNA	107
4 *A.palaestina* 2	KVVGYDSKYNCHLME	KIE--AENLLNRAFS	VFLFNSKYELLLQQR	SATKVTFPLVWTNTC	CSHPLFRDS------	--ELIEENFLGVRNA	170
5 *A.palaestina* 1	KVVGHDSKYNCHLME	KIE--AENLLHRAFS	VFLFNSKYELLLQQR	SATKVTFPLVWTNTC	CSHPLFRDS------	--ELIEENYLGVRNA	109
6 *O.sativa* 1	NVVGHESKYNCHLME	KIE--SENLLHRAFS	VFLFNSKYELLLQQR	SATKVTFPLVWTNTC	CSHPLYRES------	--ELIQENYLGVRNA	113
7 *A.thaliana* 1	RVVGHVSKYNCHLME	NIE--AKNLLHRAFS	VFLFNSKYELLLQQR	SNTKVTFPLVWTNTC	CSHPLYRES------	--ELIQDNALGVRNA	160
8 *A.thaliana* 2	RVVGHDTKYNCHLME	KIE--AENLLHRAFS	VFLFNSKYELLLQQR	SKTKVTFPLVWTNTC	CSHPLYRES------	--ELIEENVLGVRNA	109
9 *H.pluvialis* 1	NITGNASKLECHKFL	PH--QPAGLLHRAFS	VFLFDDQGRLLLQQR	ARSKITFPSVWTNTC	CSHPLHGQTPDEVDQ	LSQVADGTVPGAKAA	162
10 *H.pluvialis* 2	NITGHASKLECHKFL	PH--QPAGLLHRAFS	VFLFDDQGRLLLQQR	ARSKITFPSVWTNTC	CSHPLHGQTPDEVDQ	LSQVADGTVPGAKAA	174
11 *C.reinhardtii* 1	RLLGTANKYDCHRFE	AAKGQPCGRLHRAFS	VFLFSPDGRLLLQQR	AASKVTFPGVWTNTC	CSHPLAGQAPDEVDL	PAAVASGQVPGIKAA	174

FIG. 22A

```
                    181        195 196        210 211        225 226        240 241        255 256        270
1 T.erecta 1        AQRKLLDELGIPAED VPVDQFTPLGRMLY- --KAPSDG----KWG EHELDYLLFIVRD-- VAVNPNPDEVADIKY VSHEELKELLRKADA 188
2 L.sativa 1        AQRKLLDELGIPGAD VPVDEFTPLGRILY- --KAASDG----KWG EHELDYLLFMVRD-- VGLDPNPDEVKDVKY VNREELKELVRKADA 236
3 L.sativa 2        AQRKLLDELGIPAED VPVDEFTTLGRMLY- --KAPSDG----KWG EHEVDYLLFLVRD-- VAVNPNPDEVADIRY VNQEELKELLRKADA 188
4 A.palaestina 2    AQRKLLDELGIPAED VPVDEFTPLGRILY- --KAPSDG----KWG EHELDYLLFIVRD-- VKYDPNPDEVADAKY VNREELKEILRKADA 251
5 A.palaestina 1    AQRKLLDELGIPAED VPVDEFTPLGRILY- --KAPSDG----KWG EHELDYLLFIVRD-- VKYDPNPDEVADAKY VNREELREILRKADA 190
6 O.sativa 1        AQRKLLDELGIPAED VPVDQFTPLGRMLY- --KAPSDG----KWG EHELDYLLFIVRD-- VKVVPNPDEVADVKY VSREQLKELIRKADA 194
7 A.thaliana 1      AQRKLLDELGIVAED VPVDEFTPLGRMLY- --KAPSDG----KWG EHELDYLLFIVRD-- VKVQPNPDEVAEIKY VSREELKELVKKADA 241
8 A.thaliana 2      AQRKLFDELGIVAED VPVDEFTPLGRMLY- --KAPSDG----KWG EHEVDYLLFIVRD-- VKLQPNPDEVAEIKY VSREELKELVKKADA 190
9 H.pluvialis 1     AIRKLEHELGIPAHQ LPASAFRFLTRLHYC AADVQPAATQSALWG EHEMDYILFIRAN-- VTLAPNPDEVDEVRY VTQEELRQMMQP--- 247
10 H.pluvialis 2    AIRKLEHELGIPAHQ LPASAFRFLTRLHYC AADVQPAATQSALWG EHEMDYILFIRAN-- VTLAPNPDEVDEVRY VTQEELRQMMQP--- 259
11 C.reinhardtii 1  AVRKLQHELGIPPEQ VPASSFSFLTRLHYC AADTATHG-PAAEWG EHEVDYVLFVRPQQP VSLQPNPDEVDATRY VTLPELQSMMA---- 259

                    271        285 286        300 301        315 316
1 T.erecta 1        GEEGLKLSPWFRLVV DN--FLFKWWDHVQK GTL---TEAIDMKTI HKLI--  232  Tagetes erecta (marigold)
2 L.sativa 1        GEEGVKLSPWFKLIV DN--FLFQWWDRLHK GTL---TEAIDMKTI HKLT--  280  Lactuca sativa (romaine lettuce)
3 L.sativa 2        GEEGLKLSPWFRLVV DN--FLFKWWDHVQK GTL---NEAIDMKTI H-----  229  Lactuca sativa (romaine lettuce)
4 A.palaestina 2    GEEGIKLSPWFRLVV DN--FLFKWWDHVEE GKI---KDVADMKTI HKLT--  295  Adonis palaestina (pheasant's eye)
5 A.palaestina 1    GEEGLKLSPWFRLVV DN--FLFKWWDHVEQ GTI---KEVADMKTI HKLT--  234  Adonis palaestina (pheasant's eye)
6 O.sativa 1        GEEGLKLSPWFRLVV DN--FLMGWWDHVEK GTL---NEAVDMETI HKLK--  238  Oryza sativa (rice)
7 A.thaliana 1      GEEGLKLSPWFRLVV DN--FLMKWWDHVEK GTL---VEAIDMKTI HKL---  284  Arabidopsis thaliana
8 A.thaliana 2      GDEAVKLSPWFRLVV DN--FLMKWWDHVEK GTI---TEAADMKTI HKL---  233  Arabidopsis thaliana
9 H.pluvialis 1     -DNGLQWSPWFRIIA AR--FLERWWADLDA ALN--TDKHEDWGTV HHINEA  293  Haematococcus pluvialis
10 H.pluvialis 2    -DNGLQWSPWFRIIA AR--FLERWWADLDA ALN--TDKHEDWGTV HHINEA  305  Haematococcus pluvialis
11 C.reinhardtii 1  -DPGLSWSPWFRILA TQPAFLPAWWGDLKR RWRPGGSRLSDWGTI HRVM--  307  Chlamydomonas reinhardtii
```

FIG. 22B

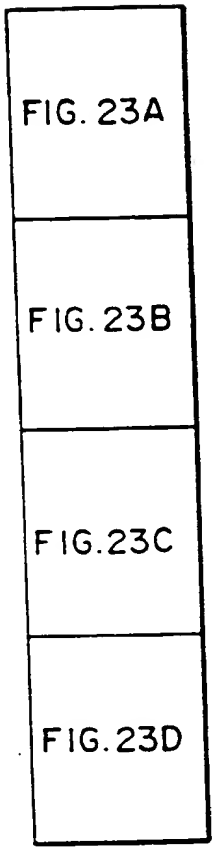

FIG. 23

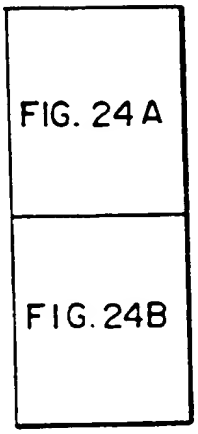

FIG. 24

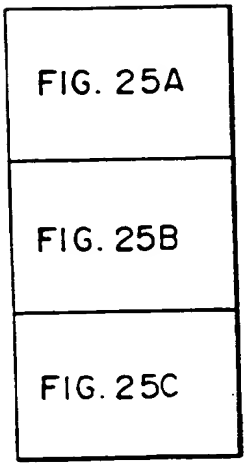

FIG. 25

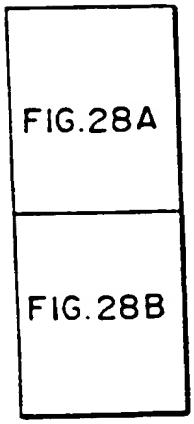

FIG. 28

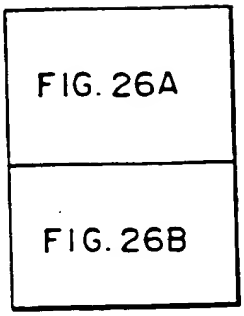

FIG. 26

FIG. 23A

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Comparison using GAP program of the Genetics Computer Group

Gap Weight:	50	Average match:	10.000
Length Weight:	3	Average Mismatch:	0.000
Quality:	17392	Length:	1904
Ratio:	9.411	Gaps:	3
Percent Similarity:	95.331	Percent Identity:	95.331

Match display thresholds for the alignment(s):
| = IDENTITY : = 5 . = 1

Adonis palaestina ε-cyclase #3 x *Adonis palaestina* ε-cyclase #5

```
  1 gagagaaaaagagtgttatattaatgttactgtcgcattcttgcaacac.  49
  1 ......aaaggagtgttctattaatgttactgtcgcattcttgcaacact  44

 50 .atattcagactccattttcttgttttctcttcaaaacaacaaactaatg  98
 45 tatattcaaactccattttcttcttttctcttcaaaacaacaaactaatg  94

 99 tga.cggagtatctagctatggaactacttggtgttcgcaacctcatctc 147
 95 tgagcagagtatctggctatggaactacttggtgttcgcaacctcatctc 144

148 ttcttgccctgtctggacttttggaacaagaaaccttagtagttcaaaac 197
145 ttcttgccctgtgtggacttttggaacaagaaaccttagtagttcaaaac 194

198 tagcttataacatacatcgatatggttcttcttgtagagtagattttcaa 247
195 tagcttataacatacatcgatatggttcttcttgtagagtagattttcaa 244

248 gtgagggctgatggtggaagcgggagtagaacttctgttgcttataaaga 297
245 gtgagagctgatggtggaagcgggagtagaagttctgttgcttataaaga 294

298 gggttttgtggacgaggaggattttatcaaagctggtggttctgagcttt 347
295 gggttttgtggatgaagaggattttatcaaagctggtggttctgagcttt 344

348 tgtttgtccaaatgcagcaaacaaagtctatggagaaacaggccaagctc 397
345 tgtttgtccaaatgcagcaaacaaagtctatggagaaacaggccaagctc 394
```

FIG. 23B

```
398 gccgataagttgccaccaatacctttcggagaatctgtgatggacttggt 447
    ||||||||||||||||||||||||||| ||||||| ||||||||||||||
395 gccgataagttgccaccaatacctttggagaatccgtgatggacttggt 444

448 tgtaataggttgtggacctgctggtctttcactggctgcagaagctgcta 497
    ||||||||||||||||||||||||||||||||||||||||||||||||||
445 tgtaataggttgtggacctgctggtctttcactggctgcagaagctgcta 494

498 agctaggcttgaaagttggccttattggtcctgatcttccttttacaaat 547
    ||||||| |||||| ||||||||||||||||||||||||||||||||||
495 agctagggttgaaagttggccttattggtcctgatcttccttttacaaat 544

548 aattatggtgtgtgggaagacgagttcaaagatcttggacttgaacgttg 597
    ||||||||||||||||||||||||||||||||||||||||||||||||||
545 aattatggtgtgtgggaagacgagttcaaagatcttggacttgaacgttg 594

598 tatcgagcatgcttggaaggacaccatcgtatatcttgacaatgatgctc 647
    ||||||||||||||||||||||||||||||||||||| ||||||||||
595 tatcgagcatgcttggaaggacaccatcgtatatcttgataatgatgctc 644

648 ctgtccttattggtcgtgcatatggacgagttagccggcatttgctgcat 697
    |||||||||||||||||||||||||||||||||||| || |||||||| |||
645 ctgtccttattggtcgtgcatatggacgagttagtcgacatttgctacat 694

698 gaagagttgctgaaaaggtgtgtcgagtcaggtgtatcatatctgaattc 747
    || |||||||||||||||||||| |||||||||||||||||||| ||||
695 gaggagttgctgaaaaggtgtgtggagtcaggtgtatcatatctggattc 744

748 taaagtggaaaggatcactgaagctggtgatggccatagtcttgtagttt 797
    ||||||||||||||||||||||||||||||||||||||| ||||||||||
745 taaagtggaaaggatcactgaagctggtgatggccatagccttgtagttt 794

798 gtgaaaacgacatctttatcccttgcaggcttgctactgttgcatctgga 847
    ||||||| || |||||||||||||||||||||||||||||||||||||||
795 gtgaaaatgagatctttatcccttgcaggcttgctactgttgcatctgga 844

848 gcagcttcagggaaacttttggagtatgaagtaggtggccctcgtgtttg 897
    |||||||||||||||||||||||||||||||||||||||||||||||||
845 gcagcttcagggaaacttttggagtatgaagtaggtggccctcgtgtttg 894

898 tgtccaaactgcttatggtgtggaggttgaggtggagaacaatccatacg 947
    ||||||||| ||||||| |||||||||||||||||||||||||||||||
895 tgtccaaaccgcttatggggtggaggttgaggtggagaacaatccatacg 944
```

FIG. 23C

```
948 atcccaacttaatggtatttatggactacagagactatatgcaacagaaa 997
    ||||||||||||||||||| ||||||||||||||||||||||||||||||
945 atcccaacttaatggtattcatggactacagagactatatgcaacagaaa 994

998 ttacagtgctcggaagaagaatatccaacatttctctatgtcatgcccat 1047
    ||||||||||||||||||||||||||||||||||||||||||||||||||
995 ttacagtgctcggaagaagaatatccaacatttctctatgtcatgcccat 1044

1048 gtcgccaacaagacttttttttgaggaaacctgtttggcctcaaaagatg 1097
     ||||||||||||||||||||||||||||||||||||||||||||||||||
1045 gtcgccaacaagacttttttttgaggaaacctgtttggcctcaaaagatg 1094

1098 ccatgcctttcgatctactgaagagaaaactaatgtcacgattgaagact 1147
     ||||||| |||||||||||||||||||| ||||||||||||||||||||
1095 ccatgccattcgatctactgaagagaaaactgatgtcacgattgaagact 1144

1148 ctgggtatccaagttacaaaaatttatgaagaggaatggtcttatattcc 1197
     |||||||||||||||||||| |||||||||||||||| ||||||||
1145 ctgggtatccaagttacaaaagtttatgaagaggaatggtcatatattcc 1194

1198 tgttgggggttctttaccaaacacagagcaaaagaacctagcatttggtg 1247
     |||||| ||||||||||||||||||||||||||||||||||||||||||
1195 tgttggtggttctttaccaaacacagagcaaaagaacctagcatttggtg 1244

1248 ctgcagcaagcatggtgcatccagcaacaggctattcggttgtacgatca 1297
     |||||||||||||||||||||||||||||||||||||||||||| |||
1245 ctgcagcaagcatggtgcatccagcaacaggctattcggttgtacggtca 1294

1298 ctatcagaagctccaaaatatgcttctgtaattgcaaagattttgaagca 1347
     || |||||||||||||||||||||||||||||||||||||||||||||
1295 ctgtcagaagctccaaaatatgcttctgtaattgcaaagattttgaagca 1344

1348 agataactctgcatatgtggtttctggacaaagcagtgcagtaaacattt 1397
     |||||||||||| |||||||| |||||||| ||||||||||||||||
1345 agataactctgcgtatgtggtttctggacaaagtagtgcagtaaacattt 1394

1398 caatgcaagcatggagcagtctttggccaaaggagcgaaaacgtcaaaga 1447
     ||||||||||||||||||||||||||||||||||||||||||||||||
1395 caatgcaagcatggagcagtctttggccaaaggagcgaaaacgtcaaaga 1444

1448 gcattctttcttttcgggttagagcttattgtgcagctagatattgaagc 1497
     |||||||||||||| || ||||||||||||||||||||||||||||||
1445 gcattctttcttttggattagagcttattgtgcagctagatattgaagc 1494
```

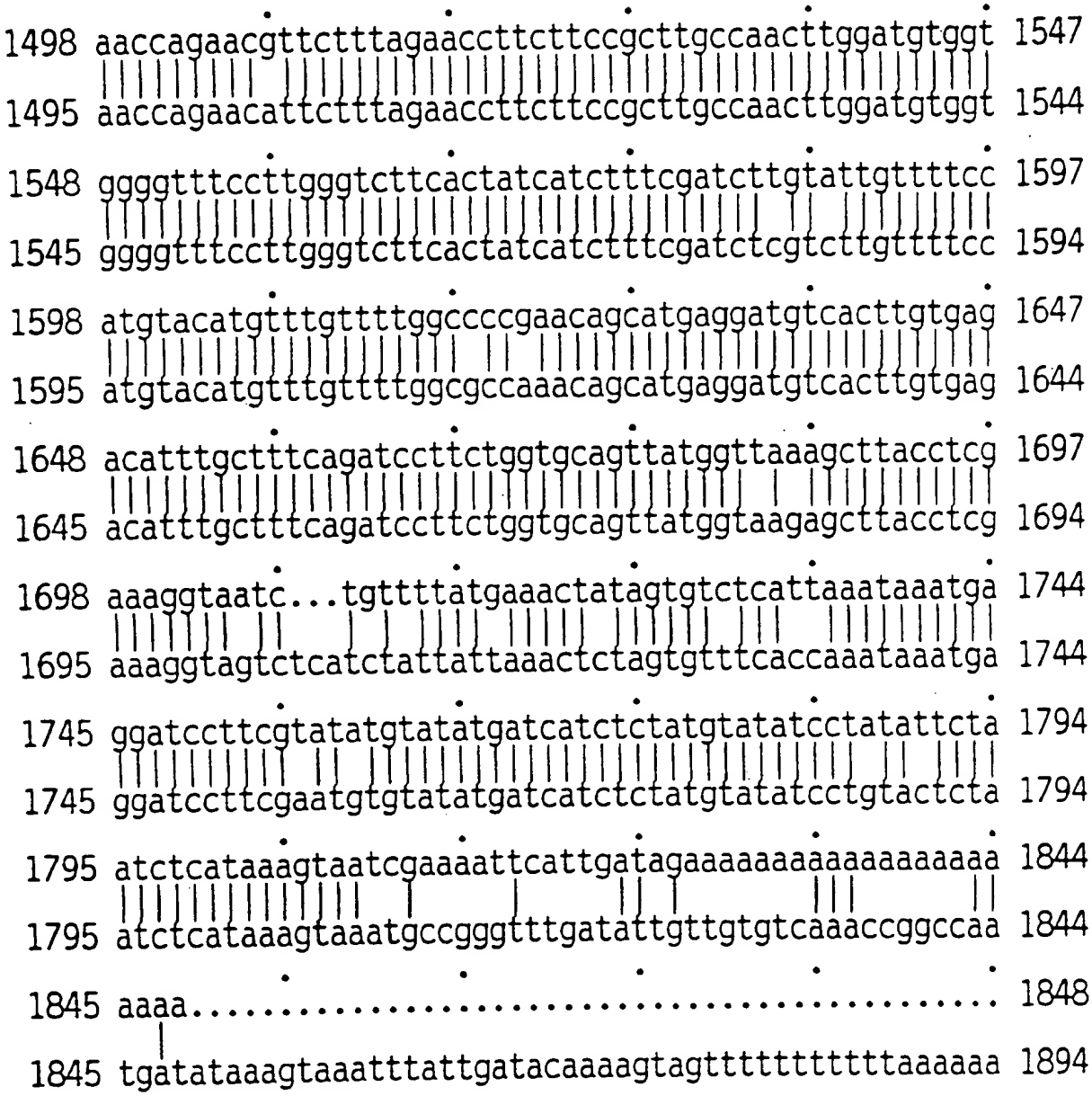

FIG. 23D

FIG. 24A

GAP program of Genetics Computer Group
blosum62.cmp

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	2728	Length:	530
Ratio:	5,147	Gaps:	0
Percent Similarity:	99,623	Percent Identity:	99.057

Match display thresholds for the alignment(s):
| = IDENTITY : = 2 . = 1

Adonis palaestina ε-cyclase #3 x *Adonis palaestina* ε-cyclase #5

```
  1 MELLGVRNLISSCPVWTFGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGG 50
    ||||||||||||||||||||||||||||||||||||||||||||||||||
  1 MELLGVRNLISSCPVWTFGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGG 50

 51 SGSRTSVAYKEGFVDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPP 100
    |||||||||||||||||||||||||||||||||||||||||||||||||||
 51 SGSRSSVAYKEGFVDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPP 100

101 IPFGESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLPFTNNYGVWE 150
    ||||||||||||||||||||||||||||||||||||||||||||||||||
101 IPFGESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLPFTNNYGVWE 150

151 DEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKR 200
    ||||||||||||||||||||||||||||||||||||||||||||||||||
151 DEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKR 200

201 CVESGVSYLNSKVERITEAGDGHSLVVCENDIFIPCRLATVASGAASGKL 250
    |||||||||||||||||||||||||:|||||||||||||||||||||||||
201 CVESGVSYLDSKVERITEAGDGHSLVVCENEIFIPCRLATVASGAASGKL 250

251 LEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDYMQQKLQCSEE 300
    ||||||||||||||||||||||||||||||||||||||||||||||||||
251 LEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDYMQQKLQCSEE 300

301 EYPTFLYVMPMSPTRLFFEETCLASKDAMPFDLLKRKLMSRLKTLGIQVT 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
301 EYPTFLYVMPMSPTRLFFEETCLASKDAMPFDLLKRKLMSRLKTLGIQVT 350
```

```
351 KIYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPK 400
    |:|||||||||||||||||||||||||||||||||||||||||||||||||||
351 KVYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPK 400

401 YASVIAKILKQDNSAYVVSGQSSAVNISMQAWSSLWPKERKRQRAFFLFG 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
401 YASVIAKILKQDNSAYVVSGQSSAVNISMQAWSSLWPKERKRQRAFFLFG 450

451 LELIVQLDIEATRTFFRTFFRLPTWMWWGFLGSSLSSFDLVLFSMYMFVL 500
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
451 LELIVQLDIEATRTFFRTFFRLPTWMWWGFLGSSLSSFDLVLFSMYMFVL 500

501 APNSMRMSLVRHLLSDPSGAVMVKAYLER* 530
    |||||||||||||||||||||||:|||||||
501 APNSMRMSLVRHLLSDPSGAVMVRAYLER* 530
```

FIG. 24B

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APPROVED BY DRAFTSMAN	O.G. FIG.	
	CLASS	SUBCLASS

FIG. 25A

```
                           *        20         *        40         *        60         *        80         *       100         *
PotatoE       : -------------------------------------------------------------------------------------------------------------- :   -
ArabidopsisE  : MECVGARNF-AAMAVSTFPSWS-CRRKFPVVKRYSYRNIRFGL-CSV--RASGGGSSGSESCVAVREDF--ADEEDFVKAGGSEILFVQMQQNKDMDEQSKLVDKLPPIS : 103
AdonisE1      : MELLGVRNL-----ISSCPVWT-FGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGGSGSRSSVAYKEGF--VDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPPIP : 102
AdonisE2      : MELLGVRNL-----ISSCPVWT-FGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGGSGSRTSVAYKEGF--VDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPPIP : 102
LettuceEE     : MECFGARNMTATMAVFTCPRFTDCNIRHKFSLLKQRRFTNLSA-SSSLRQIKCSAKSDR--CVVDKQGISVADEEDYVKAGGSELFFVQMQRTKSMESQSKLSEKLAQIP : 107
TomatoE       : MECVGVQNV-GAMAVLTRPRLN----RWSGGELCQEKSIFLAY-EQY--ESKCNSSSGSDSCVVDKEDF--ADEEDYIKAGGSQLVFVQMQQKKDMDQQSKLSDELRQIS : 100
MarigoldE     : MSMRAG-HMTATMAAFTCPRFM--------------TSIRYT------KQIKCNAAKSQ---LVVKQEI--EEEEDYVKAGGSELLFVQMQQNKSMDAQSSLSQKLPRVP :  84
ArabidopsisB  : -----------------------------MDTLLKTPNKLDFFIPQFHGFE--RLCSNNPYHSRVRLGVKKRAIKIV------SSVVSGSAALLDLVPETKKENLDFEL :  72
AdonisB       : -----------------------------MDTLLRTHNKLELLPTLHGFA---EKQHLVSTSKLQNQVFRIASRNIH--PCRNGTVKARGSALLELVPETKKENLEFDL :  75
PepperB       : -----------------------------MDTLLRTPNNLEFL---HGFG---VKVSAFSSVKSQKFGAKKFCEGLG---SRSVCVKASSSALLELVPETKKENLDFEL :  71
TomatoB       : -----------------------------MDTLLKTPNNLEFLNPHHGF----AVKASTFRSEKHHNFGSRKFCETL---GRSVCVKGSSSALLELVPETKKENLDFEL :  73
TobaccoB      : -----------------------------MDTLLKTPNKLEFLHPVHGFS---VKASSFNSVKPHKFGSRKICENWG----KGVCVKAKSSALLELVPETKKENLDFEL :  73
MarigoldB     : -----------------------------MDTFLRTYNSFEFVHPSNKFAGNLNNLNQLNQSKSQFQDFRFGPKKSQFKLGQKYCVKASSSALLELVPEIKKENLDFDL :  80
DaffodilB     : -----------------------------MDTLLRTHNRLELLYPLHELA---KRHFLSPSPNPQNPNFKFFSRKPYQKKCRNGYIGVSSNQLLDLVPEIKKEHLEFDL :  77

                     120         *       140         *       160         *       180         *       200         *       220
PotatoE       : ---------------------------------------------------DEFKDLGLQACIEHVWRDTIVYLDDDDPILIGRAYGRVSRHLLHEELLKRCVEA :  54
ArabidopsisE  : IG-----DGALDHVVIGCGPAGLALAAESAKLGLKVGLIGPDLP---FTNNYGVWEDEFNDLGLQKCIEHVWRETIVYLDDDKPITIGRAYGRVSRRLLHEELLRRCVES : 205
AdonisE1      : FG-----ESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLP---FTNNYGVWEDEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKRCVES : 204
AdonisE2      : FG-----ESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLP---FTNNYGVWEDEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKRCVES : 204
LettuceEE     : IG-----NCILDLVVIGCGPAGLALAAESAKLGLNVGLIGPDLP---FTNNYGVWQDEFIGLGLEGCIEHSWKDTLVYLDDADPIRIGRAYGRVHRDLLHEELLRRCVES : 209
TomatoE       : AG-----QTVLDLVVIGCGPAGLALAAESAKLGLNVGLVGPDLP---FTNNYGVWEDEFKDLGLQACIEHVWRDTIVYLDDDEPILIGRAYGRVSRHFLHEELLKRCVEA : 202
MarigoldE     : IGGGGDSNCILDLVVIGCGPAGLALAGESAKLGLNVALIGPDLP---FTNNYGVWEDEFIGLGLEGCIEHVWRDTVVYLDNDPILIGRAYGRVSRDLLHEELLTRCMES : 191
ArabidopsisB  : PLYDTSKSQVVDLAIVGGGPAGLAVAQQVSEAGLSVCSIDPS-PKLIWPNNYGVWVDEFEAMDLLDCLDTTWSGAVVYVDEGVKKDLSRPYGRVNRKQLKSKMLQKCITN : 181
AdonisB       : PAYDPSRGIVVDLAVVGGGPAGLAIAQQVSEAGLLVCSIDPS-PKLIWPNNYGVWVDEFEAMDLLDCLDTTWSGAVVYTDDNSKKYLDRPYGRVNRKQLKSKMLQKCVTN : 184
PepperB       : PMYDPSKGVVVDLAVVGGGPAGLAVAQQVSEAGLSVCSIDPN-PKLIWPNNYGVWVDEFEAMDLLDCLDATWSGAAVYIDDKTTKDLNRPYGRVNRKQLKSKMMQKCILN : 180
TomatoB       : PMYDPSKGVVVDLAVVGGGPAGLAVAQQVSEAGLSVCSIDPN-PKLIWPNNYGVWVDEFEAMDLLDCLDATWSGAAVYIDDNTAKDLHRPYGRVNRKQLKSKMMQKCIMN : 182
TobaccoB      : PMYDPSKGLVVDLAVVGGGPAGLAVAQQVSEAGLSVVSIDPS-PKLIWPNNYGVWVDEFEAMDLLDCLDATWSGTVVYIDDNTTKDLDRPYGRVNRKQLKSKMMQKCILN : 182
MarigoldB     : PMYDPSRNVVVDLVVVGGGPSGLAVAQQVSEAGLTVCSIDPS-PKLIWPNNYGVWVDEFEAMDLIDCIDTTWSSAVVYIDEKSTKSLNRPYARVNRKQLKTKMLQKCIAN : 189
DaffodilB     : PLYDPSKALTLDLAVVGGGPLARSCSTSLG-GGLSVVSIDPN-PKLIWPNNYGVWVDEFEDMDLIDCLDATWSGALVYVDDRSTKNLSRPYARVNRKNLKSKMMKKCVSN : 185
```

```
                    *         240         *         260         *         280         *         300         *         320         *
PotatoE       : GVLYLNSKVDRIVEATNGHSLVECEGDVVIPCRFVTVASGAASGKFLQYELGGPRVSVQTAYGVEVEVDNNPFDPSLMVFMDYRDY---VRHDAQSLEAKYPTFLYAMPM : 161
ArabidopsisE  : GVSYLSSKVDSITEASDGLRLVACDDNNVIPCRLATVASGAASGKLLQYEVGGPRVCVQTAYGVEVEVENSPYDPDQMVFMDYRDY---TNEKVRSLEAEYPTFLYAMPM : 312
AdonisE1      : GVSYLDSKVERITEAGDGHSLVVCENEIFIPCRLATVASGAASGKLLEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDY---MQQKLQCSEEEYPTFLYVMPM : 311
AdonisE2      : GVSYLNSKVERITEAGDGHSLVVCENDIFIPCRLATVASGAASGKLLEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDY---MQQKLQCSEEEYPTFLYVMPM : 311
LettuceEE     : GVSYLSSKVERITEAPNGYSLIECEGNITIPCRLATVASGAASGKFLEYELGGPRVCVQTAYGIEFEVENNPYDPDLMVFMDYRDF---SKHKPESLEAKYPTFLYVMAM : 316
TomatoE       : GVLYLNSKVDRIVEATNGQSLVECEGDVVIPCRFVTVASGAASGKFLQYELGSPRVSVQTAYGVEVEVDNNPFDPSLMFVMDYRDY---LRHDAQSLEAKYPTFLYAMPM : 309
MarigoldE     : GVSYLSSKVERITEAPNGLSLIECEGNITIPCRLATVASGAASGKLLQYELGGPRVCVQTAYGIEVEVESIPYDPSLMVFMDYRDY---TKHKSQSLEAQYPTFLYVMPM : 298
ArabidopsisB  : GVKFHQSKVTNVVH-EEANSTVVCSDGVKTQASVVLDATG-FSRCLVQYD-KPYNPGYQVAYGIVAEVDGHPFDVDKMVFMDWRDKHLDSYPELKERNSKIPTFLYAMPF : 288
AdonisB       : GVKFHQAKVIKVIH-EESKSLLICNDGITINATVVLDATG-FSRCLVQYD-KPYNPGYQVAYGIMAEVEEHPFDLDKMLFMDWRDSHLNEKLELKDKNRKIPTFLYAMPF : 291
PepperB       : GVKFHQAKVIKVIH-EESKSMLICNDGITIQATVVLDATG-FSRSLVQYD-KPYNPGYQVAYGILAEVEEHPFDVNKMVFMDWRDSHLKNNVELKERNSRIPTFLYAMPF : 287
TomatoB       : GVKFHQAKVIKVIH-EESKSMLICNDGITIQATVVLDATG-FSRSLVQYD-KPYNPGYQVAYGILAEVEEHPFDVNKMVFMDWRDSHLKNNTDLKERNSRIPTFLYAMPF : 289
TobaccoB      : GVKFHHAKVIKVIH-EEAKSMLICNDGVTIQATVVLDATG-FSRCLVQYD-KPYKPGYQVAYGILAEVEEHPFDTSKMVLMDWRDSHLGNNMELKERNRKVPTFLYAMPF : 289
MarigoldB     : GVKFHQAKVIKVIH-EELKSLLICNDGVTIQATLVLDATG-FSRSLVQYD-KPYNPGYQVAYGILAEVEEHPFDVDKMLFMDWRDSHLDQNLEIKARNSRIPTFLYAMPF : 296
DaffodilB     : GVRFHQATVVKAMH-EEEKSYLICSDGVTIDARVVLDATG-FSRCLVQYD-KPYNPGYQVAYGILAEVEEHPFDVDKMVFMDWRDSHLNGKAELNERNAKIPTFLYAMPF : 292

                    340         *         360         *         380         *         400         *         420         *         440
PotatoE       : SPTRVFFEETCLASKDAMPFDLLKKKLMLRLNTLGVRIKEIYEEEWSYIPVGGSLPNTEQKTLAFGAAASMVHPATGYSVVRSLSEAPKCAFVLANILRQNHSKNMLTSS : 271
ArabidopsisE  : TKSRLFFEETCLASKDVMPFDLLKTKLMLRLDTLGIRILKTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPKYASVIAEILREETTKQINS-- : 420
AdonisE1      : SPTRLFFEETCLASKDAMPFDLLKRKLMSRLKTLGIQVTKVYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPKYASVIAKILKQDNSAYVVSGQ : 421
AdonisE2      : SPTRLFFEETCLASKDAMPFDLLKRKLMSRLKTLGIQVTKIYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPKYASVIAKILKQDNSAYVVSGQ : 421
LettuceEE     : SPTKIFFEETCLASREAMPFNLLKSKLMSRLKAMGIRITRTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPNYAAVIAKILRQDQSKEMISLG : 426
TomatoE       : SPTRVFFEETCLASKDAMPFDLLKKKLMLRLNTLGVRIKEIYEEEWSYIPVGGSLPNTEQKTLAFGAAASMVHPATGYSVVRSLSEAPKCASVLANILRQHYSKNMLTS- : 418
MarigoldE     : SPTKVFFEETCLASKEAMPFELLKTKLMSRLKTMGIRITKTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPNYAAVIAKILGKGNSKQMLDHG : 408
ArabidopsisB  : SSNRIFLEETSLVARPGLRMEDIQERMAARLKHLGINVKRIEEDERCVIPMGGPLPVLPQRVVGIGGTAGMVHPSTGYMVARTLAAAPIVANAIVRYLGSPSSN-----S : 393
AdonisB       : SSTKIFLEETSLVARPGLRFEDIQERMVARLKHLGIKVKSIEEDERCVIPMGGPLPVLPQRVVGIGGTAGMVHPSTGYMVARTLAAAPVVAKSIVQYLGSDRSL------ : 395
PepperB       : SSNRIFLEETSLVARPGLGMDDIQERMVARLSHLGIKVKSIEEDEHCVIPMGGPLPVLPQRVVGIGGTAGMVHPSTGYMVARTLAAAPVVANAIIQYLSSERSH------ : 391
TomatoB       : SSNRIFLEETSLVARPGLRIDDIQERMVARLNHLGIKVKSIEEDEHCLIPMGGPLPVLPQRVVGIGGTAGMVHPSTGYMVARTLAAAPVVANAIIQYLGSERSH------ : 393
TobaccoB      : SSNKIFLEETSLVARPGLRMDDIQERMVARLNHLGIKVKSIEEDEHCVIPMGGSLPVIPQRVVGTGGTAGLVHPSTGYMVARTLAAAPVVANAIIHYLGSEKDL------ : 393
MarigoldB     : SSTRIFLEETSLVARPGLKMEDIQERMAYRLKHLGIKVKSIEEDERCVIPMGGPLPVLPQRVLGIGGTAGMVHPSTGYMVARTLAAAPIVAKSIIRYLNNEKSM---VAD : 403
DaffodilB     : SSNRIFLEETSLVARPGLKMEDIQERMVARLNHLGIRIKSIEEDERCVIPMGGPLPVIPQRVVGIGGTAGMVHPSTGYMVARTLAAAPIVANSIVQYLVSDSGL------ : 396
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FIG. 25B

FIG. 25C

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                     *     460      *      480      *      500      *      520      *      540      *
PotatoE       : STPS-ISTQAWNTLWPQERKRQRSFFLFGLALILQLDIEGIRSFFRAFFRVPKWMWQGFLGSSLSXADLMLFAFYMFIIAPNDMRRGLIRHLLSDPTGATLIRTYLTF-- : 378
ArabidopsisE  : ----NISRQAWDTLWPPERKRQRAFFLFGLALIVQFDTEGIRSFFRTFFRLPKWMWQGFLGSTLTSGDLVLFALYMFVISPNNLRKGLINHLISDPTGATMIKTYLKV-- : 524
AdonisE1      : SSAVNISMQAWSSLWPKERKRQRAFFLFGLELIVQLDIEATRTFFRTFFRLPTWMWGFLGSSLSSFDLVLFSMYMFVLAPNSMRMSLVRHLLSDPSGAVMVRAYLER-- : 529
AdonisE1      : SSAVNISMQAWSSLWPKERKRQRAFFLFGLELIVQLDIEATRTFFRTFFRLPTWMWGFLGSSLSSFDLVLFSMYMFVLAPNSMRMSLVRHLLSDPSGAVMVKAYLER-- : 529
LettuceEE     : KYT-NISKQAWETLWPLERKRQRAFFLFGLSHIVLMDLEGTRTFFRTFFRLPKWMWGFLGSSLSSTDLIIFALYMFVIAPHSLRMELVRHLLSDPTGATMVKAYLTI-- : 533
TomatoE       : SSIPSISTQAWNTLWPQERKRQRSFFLFGLALILQLDIEGIRSFFRAFFRVPKWMWQGFLGSSLSSADLMLFAFYMFIIAPNDMRKGLIRHLLSDPTGATLIRTYLTF-- : 526
MarigoldE     : RYTTNISKQAWETLWPLERKRQRAFFLFGLALIVQMDIEGTRTFFRTFFRLPTWMWGFLGSSLSSTDLIIFAFYMFIIAPHSLRMGLVRHLLSDPTGGTMLKAYLTI-- : 516
ArabidopsisB  : LRGDQLSAEVWRDLWPIERRRQREFFCFGMDILLKLDLDATRRFFDAFFDLQPHYWHGFLSSRLFLPELLVFGLSLFSHASNTSRLEIMTK-GTVP-LAKMINNLVQDRD : 501
AdonisB       : -SGNELSAEVWKDLWPIERRRQREFFCFGMDILLKLDLQGTRRFFDAFFDLEPHYWHGFLSSRLFLPELLFFGLSLFSHASNASRIEIMAK-GTVP-LVNMMNNLIPDTD : 502
PepperB       : -SGDELSAAVWKDLWPIERRRQREFFCFGMDILLKLDLPATRRFFDAFFDLEPRYWHGFLSSRLFLPELIVFGLSLFSHASNTSRLEIMTK-GTLP-LVHMINNLLQDKE : 498
TomatoB       : -SGNELSTAVWKDLWPIERRRQREFFCFGMDILLKLDLPATRRFFDAFFDLEPRYWHGFLSSRLFLPELIVFGLSLFSHASNTSRFEIMTK-GTVP-LVNMINNLLQDKE : 500
TobaccoB      : -LGNELSAAVWKDLWPIERRRQREFFCFGMDILLKLDLPATRRFFDAFFDLEPRYWHGFLSSRLYLPELIFFGLSLFSRASNTSRIEIMTK-GTLP-LVNMINNLLQDTE : 500
MarigoldB     : VTGDDLAAGIWRELWPIERRRQREFFCFGMDILLKLDLEGTRRFFDAFFDLEPRYWHGFLSSRLFLPELVTFGLSLFGHASNTCRVEIMAK-GTLP-LATMIGNLVRDRE : 511
DaffodilB     : -SGNDLSADVWKDLWPIERRRQREFFCFGMDILLKLDLEGTRRFFDAFFDLEPRYWHGFLSSRLFLPELVPFGLSLFSHASNTCKLEIMAK-GTLP-LVNMINNLVQDRD : 503
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FIG. 26A

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                  *       20        *       40        *       60        *       80        *      100        *
PotatoE       : -------------------------------------------------------------------------------------------------------- :  -
ArabidopsisE  : MECVGARNF-AAMAVSTFPSWS-CRRKFPVVKRYSYRNIRFGL-CSV--RASGGGSSGSESCVAVREDF--ADEEDFVKAGGSEILFVQMQQNKDMDEQSKLVDKLPPIS : 103
AdonisE1      : MELLGVRNL-----ISSCPVMT-FGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGGSGSRSSVAYKEGF--VDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPPIP : 102
AdonisE2      : MELLGVRNL-----ISSCPVWT-FGTRNLSSSKLAYNIHRYGSSCRVDFQVRADGGSGSRTSVAYKEGF--VDEEDFIKAGGSELLFVQMQQTKSMEKQAKLADKLPPIP : 102
LettuceEE     : MECFGARNMTATMAVFTCPRFTDCNIRHKFSLLKQRRFTNLSA-SSSLRQIKCSAKSDR--CVVDKQGISVADEEDYVKAGGSELFFVQMQRTKSMESQSKLSEKLAQIP : 107
TomatoE       : MECVGVQNV-GAMAVLTRPRLN----RWSGGELCQEKSIFLAY-EQY--ESKCNSSSGSDSCVVDKEDF--ADEEDYIKAGGSQLVFVQMQQKKDMDQQSKLSDELRQIS : 100
MarigoldE     : MSMRAG-IMTATMAAFTCPRFM--------------TSIRYT------KQIKCNAAKSQ---LVVKQEI--EEEEDYVKAGGSELLFVQMQQNKSMDAQSSLSQKLPRVP :  84

                   120        *      140        *      160        *      180        *      200        *      220
PotatoE       : ---------------------------------------------------DEFKDLGLQACIEHVWRDTIVYLDDDDPILIGRAYGRVSRHLLHEELKRCVEAGVL :  57
ArabidopsisE  : IG-----DGALDHVVIGCGPAGLALAAESAKLGLKVGLIGPDLPFTNNYGVWEDEFNDLGLQKCIEHVWRETIVYLDDDKPITIGRAYGRVSRRLLHEELLRRCVESGVS : 208
AdonisE1      : FG-----ESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLPFTNNYGVWEDEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKRCVESGVS : 207
AdonisE2      : FG-----ESVMDLVVIGCGPAGLSLAAEAAKLGLKVGLIGPDLPFTNNYGVWEDEFKDLGLERCIEHAWKDTIVYLDNDAPVLIGRAYGRVSRHLLHEELLKRCVESGVS : 207
LettuceEE     : IG-----NCILDLVVIGCGPAGLALAAESAKLGLNVGLIGPDLPFTNNYGVWQDEFIGLGLEGCIEHSWKDTLVYLDDADPIRIGRAYGRVHRDLLHEELLRRCVESGVS : 212
TomatoE       : AG-----QTVLDLVVIGCGPAGLALAAESAKLGLNVGLVGPDLPFTNNYGVWEDEFKDLGLQACIEHVWRDTIVYLDDDEPILIGRAYGRVSRHFLHEELLKRCVEAGVL : 205
MarigoldE     : IGGGGDSNCILDLVVIGCGPAGLALAGESAKLGLNVALIGPDLPFTNNYGVWEDEFIGLGLEGCIEHVWRDTVVYLDDNDPILIGRAYGRVSRDLLHEELLTRCMESGVS : 194
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                     *     240        *       260        *       280        *       300        *       320        *
PotatoE      : YLNSKVDRIVEATNGHSLVECEGDVVIPCRFVTVASGAASGKFLQYELGGPRVSVQTAYGVEVEVDNNPFDPSLMVFMDYRDYVRHDAQSLEAKYPTFLYAMPMSPTRVF : 167
ArabidopsisE : YLSSKVDSLTEASDGLRLVACDDNNVIPCRLATVASGAASGKLLQYEVGGPRVCVQTAYGVEVEVENSPYDPDQMVFMDYRDYTNEKVRSLEAEYPTFLYAMPMTKSRLF : 318
AdonisE1     : YLDSKVERITEAGDGHSLVVCENEIFIPCRLATVASGAASGKLLEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDYMQQKLQCSEEEYPTFLYVMPMSPTRLF : 317
AdonisE2     : YLNSKVERITEAGDGHSLVVCENDIFIPCRLATVASGAASGKLLEYEVGGPRVCVQTAYGVEVEVENNPYDPNLMVFMDYRDYMQQKLQCSEEEYPTFLYVMPMSPTRLF : 317
LettuceEE    : YLSSKVERITEAPNGYSLIECEGNITIPCRLATVASGAASGKFLQYELGGPRVCVQTAYGIEVEVENNPYDPDLMVFMDYRDFSKHKPESLEAKYPTFLYVMAMSPTKIF : 322
TomatoE      : YLNSKVDRIVEATNGQSLVECEGDVVIPCRFVTVASGAASGKFLQYELGSPRVSVQTAYGVEVEVDNNPFDPSLMVFMDYRDYLRHDAQSLEAKYPTFLYAMPMSPTRVF : 315

                    340        *       360        *       380        *       400        *       420        *       440
PotatoE      : FEETCLASKDAMPFDLLKKKLMLRLNTLGVRIKEIYEEEWSYIPVGGSLPNTEQKTLAFGAAASMVHPATGYSVVRSLSEAPKCAFVLANILRQNHSKNMLTSSSTPS-I : 276
ArabidopsisE : FEETCLASKDVMPFDLLKTKLMLRLDTLGIRILKTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPKYASVIAEILREETTKQINS------NI : 422
AdonisE1     : FEETCLASKDAMPFDLLKRKLMSRLKTLGIQVTKVYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPKYASVIAKILKQDNSAYVVSGQSSAVNI : 427
AdonisE1     : FEETCLASKDAMPFDLLKRKLMSRLKTLGIQVTKIYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPKYASVIAKILKQDNSAYVVSGQSSAVNI : 427
LettuceEE    : FEETCLASREAMPFNLLKSKLMSRLKAMGIRITRTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPNYAAVIAKILRQDQSKEMISLGKYT-NI : 431
TomatoE      : FEETCLASKDAMPFDLLKKKLMLRLNTLGVRIKEIYEEEWSYIPVGGSLPNTEQKTLAFGAAASMVHPATGYSVVRSLSEAPKCASVLANILRQHYSKNMLTS-SSIPSI : 424
MarigoldE    : FEETCLASKEAMPFELLKTKLMSRLKTMGIRITKTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSLSEAPNYAAVIAKILGKGNSKQMLDHGRYTTNI : 414

                     *     460        *       480        *       500        *       520        *       540
PotatoE      : STQAWNTLWPQERKRQRSFFLFGLALILQLDIEGIRSFFRAFFRVPKWMWQGFLGSSLSXADLMLFAFYMFIIAPNDMRRGLIRHLLSDPTGATLIRTYLTF : 378
ArabidopsisE : SRQAWDTLWPPERKRQRAFFLFGLALIVQFDTEGIRSFFRTFFRLPKWMWQGFLGSTLTSGDLVLFALYMFVISPNNLRKGLINHLISDPTGATMIKTYLKV : 524
AdonisE1     : SMQAWSSLWPKERKRQRAFFLFGLELIVQLDIEATRTFFRTFFRLPTWMWWGFLGSSLSSFDLVLFSMYMFVLAPNSMRMSLVRHLLSDPSGAVMVRAYLER : 529
AdonisE2     : SMQAWSSLWPKERKRQRAFFLFGLELIVQLDLEATRTFFRTFFRLPTWMWWGFLGSSLSSFDLVLFSMYMFVLAPNSMRMSLVRHLLSDPSGAVMVKAYLER : 529
LettuceEE    : SKQAWETLWPLERKRQRAFFLFGLSHIVLMDLEGTRTFFRTFFRLPKWMWWGFLGSSLSSTDLIIFALYMFVIAPHSLRMELVRHLLSDPTGATMVKAYLTI : 533
TomatoE      : STQAWNTLWPQERKRQRSFFLFGLALILQLDIEGIRSFFRAFFRVPKWMWQGFLGSSLSSADLMLFAFYMFIIAPNDMRKGLIRHLLSDPTGATLIRTYLTF : 526
MarigoldE    : SKQAWETLWPLERKRQRAFFLFGLALIVQMDIEGTRTFFRTFFRLPTWMWWGFLGSSLSSTDLIIFAFYMFIIAPHSLRMGLVRHLLSDPTGGTMLKAYLTI : 516
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FIG. 26B

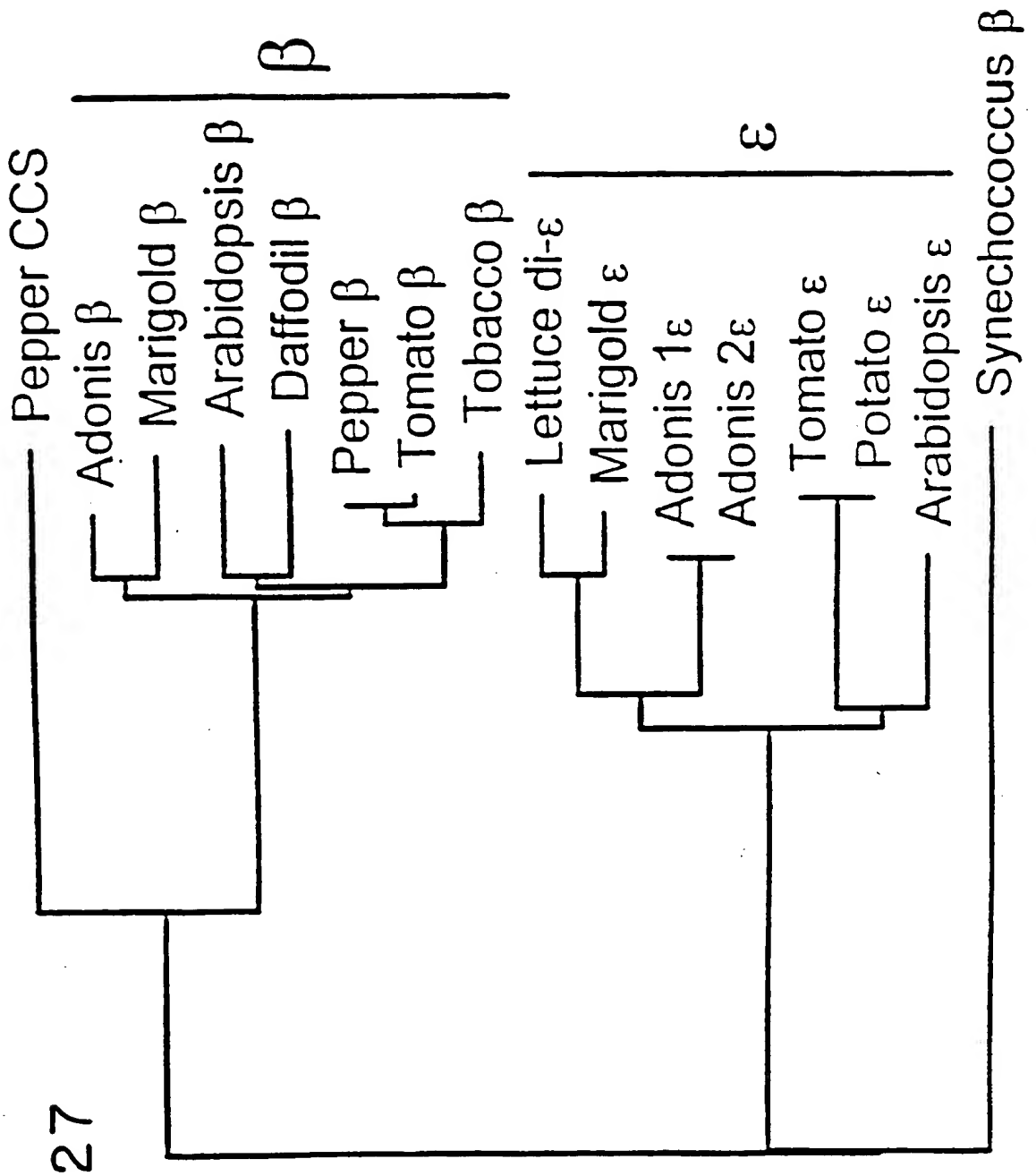

FIG. 27

FIG. 28A

GAP of: Arabidopsis epsilon cyclase to Lettuce epsilon cyclase

Gap Weight:	12	Average Match:	2.912
Length Weight:	4	Average Mismatch:	-2.003
Quality:	1837	Length:	534
Ratio:	3.499	Gaps:	3
Percent Similarity:	76.381	Percent Identity:	69.905

Match display thresholds for the alignment(s):
| = IDENTITY : = 2 . = 1

Arabidopsis x Lettuce

```
  1 MECVGARNF.AAMAVSTFPSW...SCRRKFPVVKRYSYRNIRFGLCSVRA 46
    ||| ||||  | ||| | | .  . | || ..|.  : |:       .
  1 MECFGARNMTATMAVFTCPRFTDCNIRHKFSLLKQRRFTNLSASSSLRQI 50

 47 SGGGSSGSESCVAVREDFADEEDFVKAGGSEILFVQMQQNKDMDEQSKLV 96
       |             |||||:|||||||: |||||. | |: ||||
 51 KCSAKSDRCVVDKQGISVADEEDYVKAGGSELFFVQMQRTKSMESQSKLS 100

 97 DKLPPISIGDGALDHVVIGCGPAGLALAAESAKLGLKVGLIGPDLPFTNN 146
    :||  | ||.  || ||||||||||||||||||||| ||||||||||||
101 EKLAQIPIGNCILDLVVIGCGPAGLALAAESAKLGLNVGLIGPDLPFTNN 150

147 YGVWEDEFNDLGLQKCIEHVWRETIVYLDDDKPITIGRAYGRVSRRLLHE 196
    ||||:|||  |||: |||| |::|:|||||  || |||||||| | ||||
151 YGVWQDEFIGLGLEGCIEHSWKDTLVYLDDADPIRIGRAYGRVHRDLLHE 200

197 ELLRRCVESGVSYLSSKVDSITEASDGLRLVACDDNNAIPCRLATVASGA 246
    ||||||||||||||||||: |||| .|  |: |: |  ||||||||||||
201 ELLRRCVESGVSYLSSKVERITEAPNGYSLIECEGNITIPCRLATVASGA 250

247 ASGKLLQYEVGGPRVCVQTAYGVEVEVENSPYDPDQMVFMDYRDYTNEKV 296
    ||||  |:||.|||||||||||:||||||.|||||  ||||||||:.  |
251 ASGKFLEYELGGPRVCVQTAYGIEVEVENNPYDPDLMVFMDYRDFSKHKP 300

297 RSLEAEYPTFLYAMPMTKSRLFFEETCLASKDVMPFDLLKTKLMLRLDTL 346
     ||||.||||||  | |. .::|||||||||:: |||.|||.|||  ||  :
301 ESLEAKYPTFLYVMAMSPTKIFFEETCLASREAMPFNLLKSKLMSRLKAM 350
```

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FIG. 28B

```
347 GIRILKTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSL 396
    |||| :||||||||||||||||||||||||||||||||||||||||||||
351 GIRITRTYEEEWSYIPVGGSLPNTEQKNLAFGAAASMVHPATGYSVVRSL 400

397 SEAPKYASVIAEILREETTKQINS.....NISRQAWDTLWPPERKRQRAF 441
    |||| ||.|||.|||:: .|:. |     |||:|||:|||| ||||||||
401 SEAPNYAAVIAKILRQDQSKEMISLGKYTNISKQAWETLWPLERKRQRAF 450

442 FLFGLALIVQFDTEGIRSFFRTFFRLPKWMWQGFLGSTLTSGDLVLFALY 491
    |||||. ||  | || |.||||||||||||| |||||.|.| ||::||||
451 FLFGLSHIVLXDLEGTRTFFRTFFRLPKWMWWGFLGSSLSSTDLIIFALY 500

492 MFVISPNNLRKGLINHLISDPTGATMIKTYLKV* 525
    ||||.|..||  |: ||:||||||||:| || :|
501 MFVIAPHSLRMELVRHLLSDPTGATMVKAYLTI* 534
```